

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_pzn model

Run on: January 18, 2003, 04:12:19 ; Search time 44.4279 Seconds
(without alignments)
5391.080 Million cell updates/sec

Title: US-09-026-459A-37

Perfect score: 4017
Sequence: 1 MSRLKKYDVFALFKLER.....TRMQKQKMSDMSNKEEK 781

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Processed: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_pzn.model -DEV=x1h
-O=/cgn2_1/USPTO.spool/US09026459/runat.16012003.152138.23340/app.query.fasta_1.13467
-DB=Issued Patents.NA -QEMT=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -STRAP=1 -END=1 -MATRIX=blosum62 -TRANS=hamm40.cdi
-LIST=45 -DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09026459 -ECGN_1_1.344 -runat.16012003.152138.23340 -NCPU=6 -ICPU=3
-NO_XLPEXY -NO_MAP -LANG=JQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEROUT=120
-WARN_TIMEROUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4017	100.0	2994	1	US-08-204-329-2
2	4017	100.0	2994	2	US-08-482-627-4
3	4017	100.0	2994	3	US-08-801-092-3
4	4017	100.0	2994	4	US-09-315-113-3
5	4017	100.0	2995	5	US-08-959-638-7
6	4017	100.0	3232	1	US-08-038-760-1
7	4017	100.0	3232	1	US-08-038-760-2
8	4017	100.0	3232	2	US-08-470-091-1
9	4017	100.0	3232	2	US-08-470-091-2
10	4014	99.9	2994	5	PCT-US94-10357-1
11	4007	99.8	2995	4	US-08-328-673A-7
12	768	19.1	2808	1	US-07-708-962-1

13	763	19.0	2808	2	US-08-152-721B-1
14	729.5	18.2	4853	1	US-08-832-863-1
15	729.5	18.2	4853	2	US-08-832-877-1
16	727.5	18.1	3249	1	US-08-106-493A-1
17	727.5	18.1	3249	1	US-08-429-264-1
18	516.5	12.9	3747	4	US-09-213-293D-2
19	144	3.6	6773	4	US-09-166-350-27
20	143.5	3.6	3763	1	US-07-792-865D-1
21	143	3.6	3593	4	US-09-404-627-3
22	143	3.6	4205	4	US-09-404-627-1
23	140	3.5	8789	1	US-08-328-254-5
24	138	3.4	3883	1	US-08-468-036-33
25	138	3.4	3883	2	US-08-376-843-33
26	138	3.4	3884	4	US-09-541-782-3
27	138	3.4	3884	4	US-09-723-820-3
28	138	3.4	4868	1	US-08-139-937-12
29	138	3.4	4868	5	PCT-US93-11310-12
30	137	3.4	10136	1	US-08-353-700-2
31	137	3.4	10136	5	PCT-US95-16216-2
32	131	3.3	2415	4	US-09-134-001C-2381
33	130	3.2	5893	1	US-08-592-126-54
34	130	3.2	5893	2	US-08-687-080-44
35	127.5	3.2	5181	1	US-08-257-073-10
36	126	3.1	10254	4	US-08-961-527-29
37	121	3.0	5361	4	US-08-973-462-1
38	121	3.0	6152	4	US-08-973-462-2
39	119	3.0	30549	4	US-09-134-001C-322
40	118.5	2.9	3492	4	US-08-923-992A-9
41	117.5	2.9	7493	1	US-08-212-133A-7
42	117.5	2.9	7493	1	US-08-474-503-5
43	117.5	2.9	7493	2	US-08-670-707A-5
44	117.5	2.9	7493	4	US-09-037-601-5
45	117.5	2.9	7493	4	US-09-315-179-5

ALIGNMENTS

RESULT 1
US-08-204-329-2
Sequence 2, Application US/08204329
Patent No. 5710255
GENERAL INFORMATION:
APPLICANT: SHEPARD, H. M.
APPLICANT: MEN, SHU F.
TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
TITLE OF INVENTION: MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,329
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05866
FILING DATE: 14-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: RENE A. FITTS
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 16930-00040005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 27, Appl1
Sequence 1, Appl1
Sequence 3, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 5, Appl1
Sequence 33, Appl1
Sequence 3, Appl1
Sequence 3, Appl1
Sequence 12, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 2381, Ap
Sequence 54, Appl1
Sequence 10, Appl1
Sequence 29, Appl1
Sequence 1, Appl1
Sequence 322, App
Sequence 9, Appl1
Sequence 7, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 5, Appl1

1 INFORMATION FOR SEQ ID NO: 2:
1 SEQUENCE CHARACTERISTICS:
1 LENGTH: 2994 base pairs
1 TYPE: nucleic acid
1 STRANDEDNESS: double
1 TOPOLOGY: linear
1 MOLECULE TYPE: DNA (cDNA)
1 US-08-204-329-2

Alignment Scores:

Pred. No.:	0	Length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	1	Gaps:	0

US-09-026-459A-37 (1-781) x US-08-204-329-2 (1-2994)

1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
|||||
580 ATGTCAAGACTGTGAGAGAACTATGATGTGCTGCACTCTTCAGCAAAATGGAAAG 639
QY 21 ThrCysGluLeuLeuTyrLeuThrGlnProSerSerSerLysSerThrGluLeuAsnSer 40
Db 640 ACATGTGAACCTTATATATTTGACACAAACCCAGAGTTCGATCTACTGAAATTAATTC 699
QY 41 AlaLeuValLeuLysValSerThrPheLeuLeuAlaLysGluValLeuGln 60
Db 700 GCATTGGTGCTAAAGTTTCTTGATCACAATTTTATACCTAAAGGAGATATACAA 759
QY 61 MetGluAspAspLeuValLysSerPheGlnLeuMetLeuCysValLeuAspTyrPheLe 80
Db 760 ATGGAGAGATGTATCGTGCATTTTCATTCAGTTAATGCTATGCTCTGACTATTTTAT 819
QY 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValLeuProLeuAsn 100
Db 820 AACCTCTACCTCCAGTGTCTCTAAAGAACCATTAACACAGCTTTATACCATTAAT 879
QY 101 GlySerProArgTyrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db 880 GGTTCACTCGAACACCCAGCGAGTGCACAAACGAGTGCAGATACCAAAACACATA 939
QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db 940 GAAATATGATACAGATATATTGAAGTCTCTGTAAACAAATGATATATATATAGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluLysValThr 160
Db 1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAATCTCTGAGACTGTGA 1059
QY 161 SerAsnGluLeuProGluValGluAsnLeuSerLysArgTyrGluLeuIleTyrLeuLys 180
Db 1060 TCTATATGACTTCCAGAGGTTGAAATCTTTCTAAACGATACGAAAGAAATTTATCTTAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 1120 AATAAAGATCTAGATGCAAGATATTTTTCGATCATGATGAAACCTCTCAGACGTATCT 1179
QY 201 IleAspSerPheGluThrGlnArgTyrProArgLysSerLysLeuAspGluValLysAsn 220
Db 1180 ATAGACAGTTTGGAAACCCAGAGAACCCAGAAAGATGACCTTATATAGAGAGGAGAT 1239
QY 221 ValIleProProHisIsthrProValArgThrValMetAsnThrIleGlnIleuMetMet 240
Db 1240 GTAATTCCTCCACACACTCCAGTATAGACTGTATATGACACTATCCAAACATTAATGATG 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnGly 260
Db 1300 ATTTTAAATTCAGCAAGGATGACCAACCTTCAGAAATCTGATTTTCCATTTTAAACAATCC 1359
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
|||||

Db 1360 ACAGTAATCCAAAAGATATACGAAAGAGTGAAGATATAGATATACATCTTTAA 1419
QY 281 GluLysPheAlaLysAlaValGluGlnCysValGluIleGlySerGlnArgTyrLys 300
Db 1420 GAGAAATTTGCTTAAAGCTGTGGACAGGCTGTGTCTGCAAAATGGATACACCATTCAAA 1479
QY 301 LeuGluValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
Db 1480 CTTCGAGTTCCTGTATATACCGAGTAATGCAATTCATGCTTAATTCAGAAAGAACGA 1539
QY 321 LeuSerIleGlnAsnPheSerLysLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1540 TTATCCATTCAAAATTTTATGCAAACTTCTGATATGACAAATTTTTCATATATGCTTAT 1599
QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db 1600 GCSTGCCTCTTGAGGTTGTATGTATGCGCCACATATGACAGAAAGTACATCTCAGAAATCT 1659
QY 361 SerGluThrAspLeuSerPheProTyrPheLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db 1660 TCTGAAACAGATTTGCTTCCATGATGATCTGAAATGCTTAATTTAAAGCTTTGAT 1719
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlnLysLeuThrArgGluMetIle 400
Db 1720 TTTTCAAAAGTATCGAAAGTTTATCAAGCAGAAAGCAACTGACCAAGAAATGATA 1779
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTyrLeuSerAspSer 420
Db 1780 AAACATTTGAAACGATGAGAACATGAAATCGATGATCCCTGATGCGCTCCTCAGATTC 1839
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db 1840 CCTTATTTGATCTTATTAACAAATCAAGACGAGCAAGACCAACTGATCACTTGAA 1899
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnHisIsthrAlaIleAspMetTyrLeu 460
Db 1900 TCTGCTTGCTCTTATATCTTCTCTCCAGAAATATCACTGACGACGATATATGATCT 1959
QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCCTGTATGAATCTTCAAAAGAAAAAGGTTCAACTACCGGTGAATTTACTGCAAA 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGAGACCAAGCAACTCAGCTTCCAGACCCAGAAAGCATTTGAATCTTACTCTCT 2079
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db 2080 TCACGTATTATAAAAAGTATGCGCTACCTATCTCCGGCTAAATACACTTGTGAA 2139
QY 521 ArgLeuLeuSerGluHisIsthrProGluLeuGluHisIsthrIleTyrPhePheGlnIsthr 540
Db 2140 CGCCTTCTGTGACGCCACCAATTTAGACATATCACTGTGAGCCCTTTCCAGCACACC 2199
QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db 2200 CTCAGAAATGATAGAACTCATGAGACAGAGCATTTGGACCAAAATTAATGATGTGTCC 2259
QY 561 MetTyrGluIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValIsthrAla 580
Db 2260 ATGTATGCGATATGCAAGTGAAGATATAGACCTTTAAATTCAAATCATTTGAAACGGA 2319
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db 2320 TACAAAGATCTTCATAGCTGTTCAGAGACATTTCAACGCTGTTTGAATCAAGAAAGAG 2379
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerAlaPheMetGlnArgLeuLysThrAsn 620
Db 2380 GAGTATGATTCATATATATGATATCTATTAACCTCGCTTCATGACAGACATGAAACAAAT 2439
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIsthrProArg 640
Db 2440 ATTTGCAATATAGCTTCCACAGGCCCTTACCTTGTACACATTAACCTCAGATCTCTGCA 2499

QY 281 GtlysphealalyalaValglynglyCysValgluileglySerGlnArgTyrLys 300
 Db 1420 GAGAAATTTGGCTTAAAGCTGGGACAGGTTGGTGCATAATTCGACACAGGATACAA 1479
 QY 301 LeuGlyValArgLeuTyrTyrFavValMetGluSerMetLeuLysSerGluLysArg 320
 Db 1480 CTGGAGTTCGCTTGATATACAGAGTAATGGAATCCATGGCTTAATTCAGAGAGAGCA 1539
 QY 321 LeuSerIleGlnAspPheSerLysLeuLeuAspAsnIlePheHisMetSerLeu 340
 Db 1540 TTATCCATTCATAAATTTAGCAAACTCTGAAATGACAACTTTTATATATGCTTATG 1599
 QY 341 AlaCysAlaLeuGluValAlaValMetAlaThrTyrSerArgSerThrSerGlnAsnLys 360
 Db 1600 GCGTCGCTCTGAGGTTGTAATGGCCACATATAGCAGAACTCATCATCAGAACTCTGAT 1659
 QY 361 SerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
 Db 1660 TCTGGACAGATTCTCTTCCAGGATTCGAAATGCTTAATTTAAAGCCTTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgLysMetIle 400
 Db 1720 TTTTACAAAGTATCGAAGTTTATGAAAGCAGAAAGCCAACTTCACAGACAAATGATA 1779
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTyrLeuSerAspSer 420
 Db 1780 AAACATTTAGAACCATGTGAACATCGAATCATGGATCCCTTCATGGCTTCACATTC 1839
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluLysProThrAspHisLeuGlu 440
 Db 1840 CCTTATTTTGAATCTTATTTAAACAATCAAGACCGAAGACCAACATCATCACTTGAA 1899
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaIleAspMetTyrLeu 460
 Db 1900 TCTGCTGTCCTTAACTCTCTCCAGAAATATACACTCCAGACATATGATCTT 1959
 QY 461 SerProValArgSerProLysLysGlySerThrThrArgAlaAspSerThrLysAsn 480
 Db 1960 TCTCCGTAAGATCTCCAAAGAAAAAGGTCAACTCAAGGTGTAATTTCACTCTCAAT 2019
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 Db 2020 GGAGAGACAAAGCAACCTCAGCTCCAGACCAGAACCATTTGAAATCTACCTCTCT 2079
 QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAspThrLeuGlyGlu 520
 Db 2080 TCACTGTTTATAAAAAGTATACGCTTACCTATCTCCGCTTAATACACTTTGTGA 2139
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTyrThrLeuPheGlnHisThr 540
 Db 2140 CCCCTTCGTCGTGAGACCCAGAAATAGAACATATCATCTGACACCTTTCCAGACAC 2199
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 Db 2200 CTGCAAGATGAGTATGAACTCATAGAGACAGGCAATTTGACCAATTTGATGTCTCC 2259
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
 Db 2260 ATGTATGCAATATGCAAAAGTGAACAAATATAGACCTTAATTCAAATTCATTTACACA 2319
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuLysGluGlu 600
 Db 2320 TACAGAGATCTTCCCATGCTTCAGAGACATTCACAACTGTTTGTATCAAAAGAG 2379
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 Db 2380 GAGTATGATCTATATAGTATCTATATACCTGCTTCATGAGAGACTGAAAAAAT 2439
 QY 621 IleLeuGlnTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArg 640
 Db 2440 ATTTGACAGTATGCTTCACAGGCCCTTCTGACCAATACCTACACTTCTCGA 2499
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660

Db 2500 AACCCCTTCAAGTTCCTAGTCACTCCCTTACGGATTCTCGAGGAGAACTCATATTTCA 2559
 QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
 Db 2560 CCCCTGAAGAGTCCATATTAATTTAGAGAGGTCTGCCAACCACAAACAAATGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 Db 2620 AGATCAGAAATCTTAGTATCATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTT 2679
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
 Db 2680 ATAAATTCAGATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
 Db 2740 CCTCTTAAACCACTGAAACAACTGCTTGTATTTGAAAGATCGATGAAAGCATGGA 2799
 QY 741 SerLysHisLeuProGlyLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 Db 2800 ACTAAACATCTCCAGAGAGAGTCCAAATTTACAGACAAACTGCAAAATGACTTCTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetLysAspSerMetAspThrSerAsnLysGluGlu 780
 Db 2860 CGAACACGATGCAAAAGCAAAAGTAATGATGATGATGATGATGATGATGATGATGATG 2919
 QY 781 Lys 781
 Db 2920 AAA 2922

RESULT 3
 US-08-801-092-3
 Sequence 3, Application US/08801092
 Patent No. 6074850
 GENERAL INFORMATION:
 APPLICANT: Antelman, Douglas
 APPLICANT: Gregory, Richard J.
 APPLICANT: Wils, Kenneth N.
 TITLE OF INVENTION: Tissue Specific Expression of
 TITLE OF INVENTION: Retinoblastoma protein
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 STREET: Two Embarcadero Center, 8th floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,092
 FILING DATE: 14-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/751,517
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitts, Renee A.
 REGISTRATION NUMBER: 35,136
 REFERENCE/DOCKET NUMBER: 016930-001020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 703-576-0300
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2994 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
us-08-801-092-3

Alignment Scores:

Pred. No.:	0	Length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-026-459A-37 (1-781) x US-08-801-092-3 (1-2994)

QY 1 MetSerArgLeuLeuLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
DB 580 ATGTCAAGACTGTGAAGAAGTATGATGTTGACCTCTTCAGCAATTGGAAAG 639
QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
DB 640 ACATGGAAGCTTATATTTGACACACACCAGAGTTCATCTAAGTAATTAATTTCT 699
QY 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
DB 700 GCATTGGCTAAAGTTCTTGATCACAATTTTATTAGCTAAAGGGAGATATTACA 759
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
DB 760 ATGGAAAGATGCTGTGATTTTCATTTCAGTTAATCTTGCTGCTTACATTTTATT 819
QY 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
DB 820 AAACCTGCACCTCCCATGTTGCTCAAGAACCATATAAAGCCTGTATACCCATTAAAT 879
QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
DB 880 GGTTCACTCCGAAACACCGGCGAGGTCAGAACAGAGTCACGAGTACAAACACTGA 939
QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGlnCysAsnIleAspGlu 140
DB 940 GAAATATGATCAAGATTTATGAAATTCCTCTGTAAGAACAATGATATATAGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
DB 1000 GTGAAAATGTTTATTTCAAAAATTTTATACCTTTTATGATATCTCTTGACACTTGAACA 1059
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluIleTyrLeuLys 180
DB 1060 TCTAATGACTTCCAGAGGTTGAAAATCTTCTTAACGATACGAAAGAAATTTATCTTAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
DB 1120 AATTAAGATCTAGATGCAAAATTTATTTTGATCATGATTAACCTCTCGACTGATTTCT 1179
QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
DB 1180 ATGAGACAGTTTGAACACAGACAGACACGCAAAAAGTAACCTTGATGAAGGTCGAAT 1239
QY 221 ValIleProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
DB 1240 GTAAATTCCTCCACACACTCCAGTTAGAGCTGTATGAAACCTATCCAAACAATTAATGATG 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
DB 1300 ATTTTAATTCAGCAATGATCAACCTTCAGAAAATCTGATTTCCATTTTAACAACATGC 1359
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 1360 ACAGTGAATCCAAAAGAAAGATACTGAAAAAGATGAAGATTAATGATCAATCTTTAAA 1419
QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300

DB 1420 GAGAAATTTGCTAAAGCTGTGGACAGGTTGTGCAAAATTTGATCAGCATACAA 1479
QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
DB 1480 CTTCGAGTTCCTGTTATACCGAGTAATGGAATTCATGCTTAATCAGAAAGAACGA 1539
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
DB 1540 TTATCCATTCAAAATTTTACGAAACCTCTGAAATGACAAACATTTTTCATATGCTTTAATG 1599
QY 341 AlaCysAlaLeuGluValAlaMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
DB 1600 GCGTGCGCTCTTGAGGTGTGTAATGCCATATATGCGAAGATCATCTCAGAAATCTTGAT 1659
QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
DB 1660 TCTGGAAACAGATTTGTCTTCCATGATCTGAAATGCGCTTAATTAAGACCTTTGAT 1719
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluLysAsnLeuThrArgGluMetIle 400
DB 1720 TTTTACAAAGTATCGAAAGCTTTATCAAAAGCAAGAGCAACCTTGACAGAGAAATGATA 1779
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
DB 1780 AAACATTTAGAACATGTCGAACATCGAATCATGGAATCCCTTGATGGCTCTCAGATTCA 1839
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
DB 1840 CCTTATATTTGATCTTATTAACCAATCAAGACGAGAGCAACCAATGATCACCTTGAA 1899
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnHisThrAlaAlaAspMetTyrLeu 460
DB 1900 TCTGTTCTCTCTTAACCTTCTCTCCAGATATATCCACTGACGAGATATATCTT 1959
QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
DB 1960 TCTCTGTAAAGATCTCCAAAGAAAAGGTTCACTACGCGTGAATTTACTAGCAAAAT 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
DB 2020 CGAGAGACCAAGCAACTCACCTCCAGACCCAGAAAGCAATGAAATCTCACTCTCTT 2079
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
DB 2080 TCACGTGTTTATTAATAAGTGTATCGCTAGCTATCTCCGCTTAATACATTTTGCTAA 2139
QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
DB 2140 GCGCTTGTCTGAGACACCCAGAAATTAAGAAATATCATCTGGACCTTTTCAGACACAC 2199
QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
DB 2200 CTTCGAAATAGATATGAACTCATGTAGAGACAGGCAATTTGGACCAAAATATATGATGTTCC 2259
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
DB 2260 ATGTATGGCATTTGCAAACTGAAGATATAGACCTTAATTTCAAAATATATTTGAACACA 2319
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
DB 2320 TACAAGGATCTTCCTCATCTCTTCAGAGACATTCAAACGTTTGTGATCAAAAGAGAG 2379
QY 601 GluTyrAspSerIleIleValaPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
DB 2380 GAGTATGATTCATTAATATATATTAATCTGAGCTTCATGCAAGAGAGCTGAAAAAAT 2439
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
DB 2440 ATTTTGCAATATGCTTCCACAGGCCCCCTACCTTGTCACCAATACCTCACATTTCTCGA 2499
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
DB 2500 AGCCCTTACAAAGTTTCTGATTCACCTTACGATTTCTGAGAGGAGACATATATTTCA 2559

```

QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
DB 2560 CCCCTGAGAGAGTCATATAAATTTTCAGAGAGTCTGCCAACACACACAAAAATGACTCA 2619
QY 661 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGluLys 700
DB 2620 AGATCAAGAACTTATAGTATCAATGGTGAATCATCTCGGAGCTCTGAGAAAGTTCAGAAA 2679
QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerIleGluLysSerAsn 720
DB 2680 ATAAATCAGATGATGTATACAGCAGCCGCTGCTCAAAAGAAAGTGGTGAAGGAGAAC 2739
QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly 740
DB 2740 CCTCCTAACCACCTGAAAAAACTACGCTTGATATTGAGAGATCAGATGAAGCAGATGGA 2799
QY 741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
DB 2800 AGTAAACATCTCCAGAGAGTCCAAATTTTCAGAGAAACGCGAGAAATGACCTTACT 2859
QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
DB 2860 CGAACAGCAATGCAAAAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATG 2919
QY 781 Lys 781
DB 2920 AAA 2922

RESULT 4
US-09-315-113-3
Sequence 3, Application US/09315113
Patent No. 6379927
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
Gregory, Richard J.
Wils, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of
Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOMSENDE and TOMSENDE and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,113
FILING DATE: 19-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,092
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

```

```

;
US-09-315-113-3
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
Alignment Scores:
Pred. No.: 0
Score: 4017.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
US-09-026-459a-37 (1-781) x US-09-315-113-3 (1-2994)
QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
DB 580 ATGTCAAGAGCTGTGTAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 639
QY 21 ThrCysGluLeuLeuLysLysLeuThrGlnProSerSerLysSerThrGluLysAsnSer 40
DB 640 ACATGTGAAGCTTATATATTTGACACACACAGCTGATATCTGATGATGATGATGAT 699
QY 41 AlaLeuValLeuLysValSerThrPheThrPheLeuLeuAlaLysGlyGluValLeuGln 60
DB 700 GCATTGGTCTAAAGCTTCTTGATCAGATCATTTTATAGCTAAAGGGAAGTATTACAA 759
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
DB 760 ATGGAGATGATCTGTGCTGATTTTCATTTGATTAAGTATGATGATGATGATGATGAT 819
QY 81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
DB 820 AAACCTCACCTCCATGCTGCTCAAGAACCATTTAAACAGCGTATATCCATTTAT 879
QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
DB 880 GGTTCACCTCGAACACCCAGGAGAGTCAGAACAGAGATGACGAGTACCAAAACACTA 939
QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
DB 940 GAAATGATACAGAAATATTTTGAAGTCTCTGTTAAAGACATGATGATTAATGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
DB 1000 GTGAAAAATGTTATTTCAAAAATTTTATACCTTTATGAAATTCCTTGACTGTTAACA 1059
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
DB 1060 TCTAATGACATTCAGAGAGTGAATAATCTTCTTAAACGATACGAGAAATTTATCTTAAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspIleAspLysThrLeuGlnThrAspSer 200
DB 1120 AATAAAGATCTGATGACAAATTTATTTTGGATCATGATTAACACTCTTCAACATGATCT 1179
QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
DB 1180 ATAGACAGCTTTGAAACACAGAACACACAGAACAAAGTAACTCTTGAGAGAGTGAAT 1239
QY 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnIleuMetMet 240
DB 1240 GTAATTCCTCCACACACACAGCTTGAAGCTTTATGAAACATATCCAAACATTTATATAG 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
DB 1300 ATTTTAAATTCAGCAAGTATCAACCTTCAGAAATATCGATTTCTATTGTAACAACATGC 1359
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 1360 ACAGTGAATCCAAAGAAAGATATCTGAAAAAGAGTGAAGATTAAGATACATCTTTAAA 1419
QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
DB 1420 GAGAAATTTGCTAAAGCTGTGGAGAGGTTGTGCAAAATTTGATGATCAGCATTCACAA 1479

```

```

Oy 301 LeuGIyValArgLeuTyrTyrArgValMetGlnSerMetLeuIysSerGlnGlnGluArg 320
Db 1480 CTTGGAGCTGCTGCTTATTAACGAGTATGAGATTCATGCTTAAATCAAGAAACAGAGCA 1539
Oy 321 LeuSerIleGlnAsnPheSerIysLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1540 TTATCCATTCACAAATTTTGAACAACTCGAATGCACAAATTTTTCATATGCTTATTTG 1599
Oy 341 AlacysAlaLeuGluValValMetAlaThrTyrSerIleArgSerGlnIleAsnLeuAsp 360
Db 1600 GCGTGGCTCTTGAAGTTGATATGCGCACATATGCGAAGATCATCTCAGAAATCTGAT 1659
Oy 361 SerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db 1660 TCTGGAAACAGATTGTCCTTCCATGATGATCTGAAATGCTTAAATTTAAAGCCCTTGAT 1719
Oy 381 PheTyrIysValIleGlnSerPheIleLysAlaGlnGluLysAsnLeuThrArgGlnMetIle 400
Db 1720 TTTTACAAAGTCGATCGAAAGTTTATCAACAGACAGACCACTTGACAAAGCAATGATA 1779
Oy 401 LysHisLeuGlnArgCysGlnHisArgIleMetGlnSerLeuAlaThrLeuSerAspSer 420
Db 1780 AAAACATTTAGACAGATGTGACATCGAATCGAATCCCTGATGCGCTCGACATTC 1839
Oy 421 ProLeuPheAspLeuIleLysGlnSerIysAspArgGlnGluIleProThrAspHisLeuGln 440
Db 1840 CTTTATTTGATCTTATTTAAACATCAAGAGACGAGAGACCACTGATCCCTGAA 1899
Oy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db 1900 TCTGCTGTCCTTATATCTTCTCCTCCAGATATACATCGAGAGCATATGATGTCWT 1959
Oy 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCTGTAAGATCTCCAAAGAAAAAGGTTCACTACGCGTGAATTTCTACTGCAAT 2019
Oy 481 AlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GAGAGACACAGACACCTCAGCTTCAGACCCAGACCAAGACATTTGAAATCTACTCTCT 2079
Oy 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGln 520
Db 2080 TCACGTGTTTATATAAAAAAGTATCGGCTATCCGCTATCCCGCTAAATATACATTTGTGAA 2139
Oy 521 ArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIleThrPheLeuPheGlnHisThr 540
Db 2140 CGCCTTGCTGTGAGCACCCAGAAATTAGAACATATCATCTGGACCTTTCCAGACACCC 2199
Oy 541 LeuGlnAsnGluTyrArgIleuMetArgAspArgHisIleAspGlnIleMetMetCysSer 560
Db 2200 CCGCAGAAATGAGTGTGAACTCATGAGAGACAGGCAATTTGGACCAAAATTAATGATGTCTCC 2259
Oy 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db 2260 ATGTATGGCATATGCAAGAGAGATATAGACCTTAAATTTCAAAATCATATTCACAGCA 2319
Oy 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGlnGlu 600
Db 2320 TACAAGGATCTTCTCATGCTGTTGAGAGACATTCAAACGCTTTTGTGATCAAGAAAG 2379
Oy 601 GlnTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnAlaGlnLeuLysThrAsn 620
Db 2380 GAGTATGATTTCTATATAGATCTTATACCTGGCTTCATGCGAGAACAGCAAAACAAAT 2439
Oy 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTTGGAGATGCTTCCACACAGGCCCTTACCTGTGTACCAATACCTCCATTTCCCGCA 2499
Oy 641 SerProTyrLysPheProSerSerProLeuArgIleProGlnGlyAsnIleTyrIleSer 660
Db 2500 ACCCTTACAAAGTTTCTTACTATCCCTTACGATTCCTGAGAGGACATCATATATTCTA 2559
Oy 661 ProLeuLysSerProTyrLysIleSerGlnGluLysLeuProThrProThrLysMetThrPro 680

```

```

Db 2560 CCGCTGAAGGTCATATATAATTTTCAAGAGTCTGCAACACCAACCAAAATGACTCTCA 2619
Oy 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGlnLysPheGlnLys 700
Db 2620 AGATCAAGAAATCTTATATATCAATATGTTGTAATCATATGCGGACTTCTGACAAAGTCCAGAAA 2679
Oy 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGlnLysSerAsn 720
Db 2680 ATTAATCATGATGTATGTATACAGCAGCCGCTGCTCAAAAAGAAAGTCTGAAGAAAGCAAC 2739
Oy 721 ProTyrLysProLeuLysLysLeuArgPheAspIleGlnGlySerAspGlnAlaAspGly 740
Db 2740 CCTCTTAAACCACTGAAAAAACTACGCTTGTATTTGAAAGATCATATGACAGCAATGGA 2799
Oy 741 SerLysHisLeuProGlnLysLysSerLysPheGlnGlnLysLeuAlaGlnMetThrSerThr 760
Db 2800 AGTAAACATCTCCAGAGAGTCCAAATTTCCAGCAGAACTGCGCAAAATGACTTCTACT 2859
Oy 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlnLys 780
Db 2860 CGAACAGAAATGCAAAAGCAAAATGAAATGATGATGATGATACCTCAAAACAGAGAAAG 2919
Oy 781 Lys 781
Db 2920 AAA 2922

RESULT 5
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wills, Ken N.
; APPLICANT: Maneval, Daniel C.
; TITLE OF INVENTION: Recombinant Adenoviral Vector and
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,638
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,673
; FILING DATE: 25-OCT-1994
; APPLICATION NUMBER: US 08/233,777
; FILING DATE: 19-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/142,669
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CJ 1192
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2995 base pairs
; TYPE: nucleic acid

```

```
STRANDEDNESS: single
TOPOLOGY: Linear
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2922
US-08-959-638-7

Alignment Scores:
Pred. No.: 0
Score: 4017.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 2995
Matches: 781
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-026-459a-37 (1-781) x US-08-959-638-7 (1-2995)
QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
580 ATGTCAAGACGTGTGACAGACGTATGTGTGCTCTCTCAGCAATTCGAAAGC 639
QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
640 ACATGTGACATATATATTATTCACACACACAGCATGTTCATCTACGAAATTAATTC 639
QY 41 AlaLeuValLeuLysValSerTyrIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
700 GCATGTGCTTAAAGATTCTTGATCACAATTTTATTTAGCTTAAAGGGGAAATTTTACA 759
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
760 ATTCGAAGATGATCGTATGATTTCAATTCATGCTATGCTCTCTCTCTCTCTCTCTCTCT 819
QY 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
820 AAATCTCTCACCCTCCATGCTCTCAAGAACCATATTAACACGCTTATATCCATTAAT 879
QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
880 GGTTCACCTCGAACACCCAGGCGAGGTCNANAGSAGTGCAGATGCAAAACAACTA 939
QY 121 GluAsnAspThrArgIleIleGlnValLeuCysGluHisGlyCysAsnIleAspGlu 140
940 GAATAATGATACAAAGATTTATGAAATTCCTGTGAAAGAACATGAATTAATATGATGAG 999
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
1000 GTGAAAAAATGTTATTTCAAAAAATTTTATACCTTTATGAAATTTCTCTGGACCTGTAA 1059
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
1060 TCTAATGACCTCCAGAGGTGAAATCTTTTAAACGATACGAAATTAATCTTAA 1119
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
1120 AATAAAGATCTAGATGCAAGATTAATTTTGATCAAGATAAATCTTCCACAGCATTC 1179
QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
1180 ATGAGACAGTTTGAACACAGACAAACACACGAAAGAAAGTAAACCTTGATGAGAGCTGAA 1239
QY 221 ValIleProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
1240 GTAAATCTCCACACACTCCAGTTAGGATGATTAACACATATCAACATTAATATG 1299
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
1300 ATTTTAATTCAGCAAGATGATCAACCTTCGAAAAATCTATATTCCTATTTAAACACTGC 1359
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
1360 ACAGTAATCAAAAGAAAGATTAAGTAAAGAGTAAAGATTAAGTAAATCAATCTTTAA 1419
```

```
QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
1420 GAGAAATTTGCTAAAGCTGTGGACAGGGTGTGTCAAAATTTGAAACACAGCAATCAA 1479
QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
1480 CTTGAGTTCGCTTGTATTAACGAGTAATGGAATCCATGCTTAATCAAGAAAGAACGA 1539
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
1540 TTATCCATCAAAATTTTGAACAACTCTGAAATGCAACAACTTTTCATATGCTTATATG 1599
QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
1600 GGTTCGCTCTGATGATGTATATGACCATATATAGCAAGATTCATCTCAATCTGTAT 1659
QY 361 SerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
1660 TCTGCAACAGATTTTGTCTTCCATGCAATCTGAATGTCTTAATTAAGCCCTTGTAT 1719
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGlnGlyAsnLeuThrArgGluMetIle 400
1720 TTTTCAAAAGTANTCGAAAGTTTATCAAAAGCAAGACAACTTGACAAAGAAATGATA 1779
QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTyrLeuSerAspSer 420
1780 AAACATTTAGACAGATGACATCAATCAATGAAATCCCTGCATGCTCTCAATTTCA 1839
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluLysProThrAspHisLeuGlu 440
1840 CTTTATTTGATCTTATTAACAAATCAAGACCCAGAACACCAACCACTATACCTGTAA 1899
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaIleAspPheTyrLeu 460
1900 TCTGCTGTCTCTTATCTTCTCTCTCCAGAAATATACACTCGACACATATGATCTT 1959
QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrLysAsn 480
1960 TCTCTGTGAAGATCTCCAAAGAAAGAAAGTTCAACCTACGCGGTAAATCTCTGCAAT 2019
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
2020 GCAGAGACACAGCAACCTCAGCTTCCAGACCCAGAAAGCAATTAATTAATCTCTCT 2079
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
2080 TCACGTGTTTATTAAGAAAGTATGAGCTGACCTATCTCCGCTTAATACATTTGTGAA 2139
QY 521 ArgLeuLeuSerGluHisProGluLeuGlnHisIleIleThrPheLeuPheGlnHisThr 540
2140 CGCCTTGTCTGTGACACCCAGAAATTAAGACATATCATCTGAGACCTTTTCCAGCACAC 2199
QY 541 LeuGlnAsnGluTyrGluLeuMetLysAspArgHisIleAsnAspGlnIleMetMetCysSer 560
2200 CTGCAAGATGATGATGACTCATGACAGACAGCAAGCAATTTGCAAAATTAATGATGCTCC 2259
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
2260 ATGATATGCAATTCGAAGATGAAGATTAACCTTAATTAATCAATTTCAACACACA 2319
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGlnGlu 600
2320 TCAAGAGATCTCTCATGCTCTGTCAGAGACATTCAAAGSTTTTGTATCAAAAGAGAG 2379
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetIleAsnLeuLysThrAsn 620
2380 CAGATATGATCTATATATGATATCTATATACCGGTCTTCAACAGACATGCAAAACAAAT 2439
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
2440 ATTTTGAAGTATGCTTCCACAGGCCCTTACCTTGCACCAATATCACTTCTCTGA 2499
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
```

```

Db 2500 AGCCCTTACAGATTTCCTAGTTACCCCTTACGATTCCGAGGAGACATCTAATATTTTCA 2559
Qy 661 ProLeuylSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
Db 2560 CCCCTGAAGAGTCCATATAAATTTCAGAAAGCTCTCCACACCAACAAAATGACTCCA 2619
Qy 681 ArgSerArgIleLeuValSerIleGlyGlySerPheGlyThrSerGluLysPheGlnLys 700
Db 2620 AGATCAAGAACTTAGTATCATTAATGGTGATATTCGGGACTTCGAGAGACTCCAGAAA 2679
Qy 701 IleAsnGlnMetValCysAsnSerAspArgValIleuLysArgSerAlaGluGlySerAsn 720
Db 2680 ATAAATCAGATGATATTAACACGACCGCTGCTCTCAAAAGAGTCTGAAAGAACGAC 2739
Qy 721 ProProLysProLeuLysLysIleuArgPheAspIleGluGlySerAspGluAlaAspGly 740
Db 2740 CCTCTAAACACCTGAAAAAACTACGCTTGTGATTTGAAAGATCAGATGACAGCATGGA 2799
Qy 741 SerLysHisLeuProGlyGlySerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
Db 2800 AGTAAACATCTCCAGSAGAGTCCAAATTTCAACAGAAACTGGCAGAAATGACTTCTACT 2859
Qy 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
Db 2860 CGAACACGAATGCAAAAGACGAAAAATGAATGATAGCATGATACCTCAAGACAGGAAGAG 2919
Qy 781 Lys 781
Db 2920 AAA 2922

RESULT 6
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Hu, Hong-Ji
; APPLICANT: Xu, Shi-Xue
; APPLICANT: Benedicte, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE: 19930325
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Polsant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA

```

```

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-038-760-1
Alignment Scores:
Pred. No.: 0
Score: 4017.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Caps: 0
US-09-026-459a-37 (1-781) x US-08-038-760-1 (1-3232)
Qy 1 MetSerArgLeuLeuLysLysTyrAspValIleuPheAlaLeuPheSerLysLeuGluArg 20
Db 124 ATGTCAACAGCTGTTCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
Qy 21 ThrCysGluLeuIleTyrIleuThrGlnProSerSerSerSerSerSerSerSerSerSer 40
Db 184 ACATGTGAACTTAATATTTGACACAAACCGAGTTCGATCTACTGTAATTAATTAATCT 243
Qy 41 AlaLeuValIleuLysValSerTrpIleThrPheLeuLeuAlaLysGlyLysValIleuGln 60
Db 244 GCATTGGTCTAAAAAGTTCTTGATCATATTTTATTAAGCTAAAGGAGGAGATTAACA 303
Qy 61 MetGluAspAspIleuValIleSerPheGlnLeuMetLeuLysValIleuAspTyrPheIle 80
Db 304 ATGGAAGATGATCTGGTGATTTTCATTTTCATTTTCATTTTCATTTTCATTTTCATTTTCAT 363
Qy 81 LysLeuSerProProMetLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db 364 AAACCTCACCCTCCACATGCTCTCAAGAAACCATATAAAGACCTGTATACCATTAAT 423
Qy 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db 424 GGTTCACCTCGAACACCCAGGCGAGTCAACACGAGGTGCACGGATACCAAAACACACTA 483
Qy 121 GluAsnAspThrArgIleIleGluValIleuLysGlyGlnIleGlnLysAsnIleAspGlu 140
Db 484 GAAATGATACAGAAATATATGAAGTTCTCTGTAAGAACATGATATATATATATATATATAT 543
Qy 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetLeuSerLeuLysValIleThr 160
Db 544 GTGAAAAAGTTTATTAATAAATTTTATACCTTTATGAAATTTCTTGACCTTGTAAACA 603
Qy 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGlnIleTyrIleuLys 180
Db 604 TCTAATGACCTCCAGAGCTTGAAATCTTTCTAAGACATACAGAAATTAATCTTAA 663
Qy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 664 AATTAAGATCTAGATGACAGATTAATTTTGTATGATGATTAAGAACTCTTCAAGCTAATCT 723
Qy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGlnIleValAsn 220
Db 724 ATAGACAGTTTGAACACAGACAGAACACACGAAAAAGATACCTTGATGAAAGGTGAT 783
Qy 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnIleuMetThr 240
Db 784 GTAAATTCCTCCACACCTCCAGTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 843
Qy 241 IleuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnLys 260
Db 844 ATTTTAATTCAGCAAGATCAACCTTCAGAAATCTGATTTCCATTAATTAACAACG 903
Qy 261 ThrValAsnProLysGlySerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db 904 ACAGTGAATCCAAAAGAAATATCTGAAAAGATGAAGATATAGATATAGATATAGATATAGAT 963
Qy 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300

```

Db 964 GAGAAATTTGCTAAAGCTGTGGACAGGGTTGTGCAAAATGGATCACAGCATACAAA 1023
 QY 301 LeuGluValArgLeuTyrTyrArgValMetGluSerMetLeuysSerGluGluGluArg 320
 Db 1024 CTTGGAGTTCGGTGTATACCGAGTAAAGGAAATCCATGCTTAAATCAGAAAGAACGA 1083
 QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
 Db 1084 TTATCCATTTCAAAATTTTACCAAACTCTGATATGACAACTTTTTCATATGTCCTTATTTG 1143
 QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerGlnSerGlnAsnLeuAsp 360
 Db 1144 GCGTCCGCTTTGAGGTTGTATATGCCATATATAGCAGAAATGTCATCTCGAAATCTTGAT 1203
 QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuysAlaPheAsp 380
 Db 1204 TCTGGACAGATTTGCTTTCCCATGATCTGTGAATGCTTATATTTAAAGCTTTGAT 1263
 QY 381 PheTyrIysValIleGluSerPheIleLysAlaGluGluLysAsnLeuThrArgGluMetIle 400
 Db 1264 TTTTTCAAAGTATGCAAAAGTTTATATCAAAAGCAGAAAGCAACTTGACAGAAAGAAATGATA 1323
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
 Db 1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTCATGGCTCTCAGATTCGA 1383
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGluTrpThrAspHisLeuGlu 440
 Db 1384 CCTTATTTGATCTTATTAACAATCAAGACCGAAGACGACCAAGCACTGATCCCTTGAA 1443
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
 Db 1444 TCTGCTTGCCCTTAATCTCTCTCTCCAGATATATCACACTCAGAGATATGATCTT 1503
 QY 461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
 Db 1504 TCTCCTGTAGATCTCCAAAGAAAAAGTTCAACTACGCGTGAATTTCTACGCAAT 1563
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuysSerThrSerLeu 500
 Db 1564 GCGAGACCAACCAAGCACTCAGCTCCAGCCAGCAAGCAATGCAATCTACCTCTCT 1623
 QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 Db 1624 TCACGTGTTTAAATAAAGTGTATCGGTACCTATCTCCGGCTAAATACACTTTGTGA 1683
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
 Db 1684 CCGCTTCTGCTGACACCCAGAAATAGAACATATCATCTGGAACCTTTTCCAGCACACC 1743
 QY 541 LeuGlnAsnGluTyrGluLeuMetLArgAspArgHisLeuAspGlnIleMetLecCysSer 560
 Db 1744 CTGCGAATAGATNGAAGCATGAGAGACAGCATTTGGACCAAAATTAATGATGTTC 1803
 QY 561 MetTyrGlyLecLysLysValLysAsnIleAspLeuysPheLysIleIleValIleAla 580
 Db 1804 ATGTATGGCATATGCAAAAGTAAATATATACCTTAATTAATTAATTAATTAATTAATTA 1863
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 Db 1864 TACAAAGATCTTCCATCGCTTCAGAGACGATTCAAAGCTGTTTGAACAAAGAAAG 1923
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 Db 1924 GAGTATGATCTAT 1983
 QY 621 IleLeuGlnIleTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArg 640
 Db 1984 ATTTTGCAATAGCTTCCACAGGCCCCCTACCTGTGCACCAATACCTACATCTCTCGA 2043
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 Db 2044 ACCCCTTACAGATTTCTAGTTCAACCCCTTACGATTCCTGAGAGAAACATATATTTCA 2103

QY 661 ProLeuLysSerProTyrIysIleSerGluGluLeuProThrProThrLysMetThrPro 680
 Db 2104 CCCCTGAAGATCCATATATATATTTTCAAGAGTGTGCAACACCAACAAATAATGATCTCA 2163
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 Db 2164 AGATCAAGATCTTATGTAACAATGTTGTAACAATTCGCGGACTTGTGAGAAAGTTCCAGAAA 2223
 QY 701 IleAsnGluMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGluSerAsn 720
 Db 2224 ATTAATCAGATGTGTATACAGCCAGCCAGCTGTGCTCAAAAGAAATGCTGAGAGAACCAAC 2283
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
 Db 2284 CCTCCAAACCACTGAAAAAACTACGCTTGTATATGTAAGATCATGATGAAGCATGGA 2343
 QY 741 SerLysHisLeuProGlyLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 Db 2344 AGTAAACATCTCCAGAGAGATCCAAATTTTCAGCAGAAACTGCGAGAAATGACTTCTACT 2403
 QY 761 ArgThrArgMetGluLysGlnLysMetLysAspSerMetAspTrpSerAsnLysGluGlu 780
 Db 2404 CGAACACGATGCAAAAGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2463
 QY 781 Lys 781
 Db 2464 AAA 2466
 RESULT 7
 US-08-038-760-2/c
 ; Sequence 2, Application US/08038760
 ; Patent No. 5456731
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Hong-Ji
 ; APPLICANT: Hu, Shi-Xue
 ; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
 ; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/038,760
 ; FILING DATE: 19930325
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Poissant, Brian M
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 7409-025-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8664
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3232 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: DNA
 ; US-08-038-760-2

Alignment Scores:

Pred. No.: 0 Length: 3232
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-026-459a-37 (1-781) x US-08-038-760-2 (1-3232)

QY 1 MetSerArgLeuLeuLysLysTyrAspValIleuPheAlaLeuPheSerLysLeuGluNar 20
 |||||
 Db 3113 ATGCAAGACTGTTGGAAGAGTATGATGATGTTGGCAGCTTTCAGCAAAATGGAAAG 3034
 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerLysSerThrGluIleAsnSer 40
 |||||
 Db 3053 ACAATGTAACCTTATATATTTGACACCAACCAGTTCATATCTACGAAATAAATCT 2994
 QY 41 AlaLeuValIleuLysValSerTrieThrPheLeuLeuAlaLysGluValIleuGln 60
 |||||
 2993 GCATGGTGCTAAAGTTCTTGGATCCACATTTTATAGCTAAAGGGGAAGTATTACAA 2934
 61 MetGluAspLysLeuValIleSerPheGlnLeuMetLysValIleuAspTyrPheIle 80
 |||||
 Db 2933 ATGGAAGATGATCTGGTGAATTCATTTCAATTAATGCTATGTCTTGACTATTTAT 2874
 QY 81 LysLeuSerProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
 |||||
 Db 2873 AATCTTCACCTCCCATGTTGCTCAAGAACATATAAACAGCTGTTATACCCATATAT 2814
 QY 101 GlySerProArgThrProArgArgGluGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 |||||
 Db 2813 GGTCACCTCGAACCACCGAGCGAGTCAAGACAGAGTGCAGGATGCAAAACACTA 2754
 QY 121 GluAsnSerPheArgIleIleGluValIleuCysLysGluLysGluCysAsnIleAspGlu 140
 |||||
 Db 2753 GAAATATATCAAGAAATATATGAGTCTCTGTAAAGAACATGATATATATATGATGAG 2694
 QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr 160
 |||||
 Db 2693 GTGAAATGTTATATTTCAAAATTTTATACCTTTTATCAATTTCTTGAGCTGTAA 2634
 QY 161 SerAsnGlyLeuProGluValIleGluAsnLeuSerLysArgTyrGluIleIleTyrLeuLys 180
 |||||
 Db 2633 TCTAATGACTTTCAGAGAGTGTGAATCTTTCTAAACGATACGAAGAAATTTATCTTAA 2574
 QY 181 AsnLysAspLysAlaArgLeuPheLeuAspPheLysAspLysThrLeuGlnThrAspSer 200
 |||||
 Db 2573 AATTAAGATCTAGATGAGAGATTTATTTTGGATCATGATAAACCTTCACAGCTGATCT 2514
 QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
 |||||
 Db 2513 ATACACAGTTTTCAGACACAGACAGACACCAACCAAAAGTAACTTCATGAAAGAGCTGAT 2454
 QY 221 ValIleProIleThrProValIleGlnThrValIleMetAsnThrIleGlnIleuMet 240
 |||||
 Db 2453 GTAAATTCCTCCACACACTCCAGTTAGACTGTATTAACAACATATCAACATTTATGATG 2394
 QY 241 IleuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAspCys 260
 |||||
 Db 2393 ATTTAAATTCAGCAAGTATCACTTCAGAAATTCGATTTCTATTTTAAACAGCTGC 2334
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGluTyrIlePheLys 280
 |||||
 Db 2333 ACAGTGAATCCAAAGAAATATATGAAAGAGTGAAGAGATATGATATACATCTTTAA 2274
 QY 281 GluLysPheAlaLysAlaValIleGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 |||||
 Db 2273 GAGAAATTTGCTAAAGCTGTGGAGAGGGGTGTGTGGAATTTGGATCCAGAGATACAAA 2214
 QY 301 LeuGlyValArgLeuTyrTyrArgValIleMetGluSerMetLeuLysSerGluGluNar 320
 |||||
 Db 2213 CTTGGAGTCTGCTTGTATATACGAGTAATGGAATCATGCTTAATTCAGAAAGAAAGCA 2154

QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeu 340
 |||||
 Db 2153 TTATCCATTCCAAAATTTTAGCAAACTTTCATATGACACACATTTTCAATATGCTTTATG 2094
 QY 341 AlaCysAlaLeuGluValValMetAlaIleTyrSerArgSerThrSerGlnAsnLeuAsp 360
 |||||
 Db 2093 GCGTCCGCTCTGAGGTGTATATGCCCACATATATGACAGAAATGATCATCTCGAATCTGAT 2034
 QY 361 SerGlyThrAspLeuSerPheProTrieIleuAsnValIleuAsnLeuLysAlaPheAsp 380
 |||||
 Db 2033 TCTGGAACAGATTTGCTCTTCCATGATCTCAATGCTCATATTTAAACCTTTGAT 1974
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluValAsnLeuThrArgGluMetIle 400
 |||||
 Db 1973 TTTTCAAAAGTGATCGAAAGTTTATCAAAAGCAGAAAGCACTTGACAGAGAAATGATA 1914
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaThrLeuSerAspSer 420
 |||||
 Db 1913 AATCATTTNAGAACGATGGAACATCGAATCATGGAATCCCTTCATAGCTTCACATTTCA 1854
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 |||||
 Db 1853 CCTTATTTGATCTTATTAACAATCAAGAGACGAGAAAGCAACTGATCACCTTGAA 1794
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaLysMetTyrLeu 460
 |||||
 Db 1793 TCTGCTTCTCTTATCTTATCTCTCCACAAATATATCACCTGACACATATATGATCTT 1734
 QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
 |||||
 Db 1733 TCTCTGTAAATGATCTCAAGAAAGAAAGTTCAACTACGCGGTAAATCTACTCAAT 1674
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 |||||
 Db 1673 GAGAGACACAAAGCACTCAGCTTCCAGACCCAGAGCCATGTGAATCTACCTCT 1614
 QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 |||||
 Db 1613 TCACGTGTTTAAAAAAAGTGTATCGCGTACCTATCTCCGCTTAATACACTTTGTGA 1554
 QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIlePheThrLeuPheGlnHisThr 540
 |||||
 Db 1553 GCGCTTCTGTGAGCACCCAGAAATTTGAACATATCTCTGAGCCCTTTTCCAGCACCC 1494
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 |||||
 Db 1493 CTGCAAGATGAGTATGAACATCATGAGAGACAGCAATTGGACCAATTTATGATGTGCC 1434
 QY 561 MetTyrGluIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
 |||||
 Db 1433 ATGTATGCAATATGCAAAAGTCAAAATATATGACCTTAAATTCAAATTCATTTACAGCA 1374
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValIleuIleLysGluGlu 600
 |||||
 Db 1373 TACAAGGATCTTCTCATAGCTGTGACAGAGACATTCAAACGTGTTTGTGATCAAAAGAG 1314
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 |||||
 Db 1313 GAGTATGATCTATATATATATTTCTATATCTGCTCTCATGAGAGACTGAAACCAAT 1254
 QY 621 IleuGlnIleTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 |||||
 Db 1253 ATTTTGCAGTATGCTCCACAGGCCCTTACCTTGACACCAATATCTCACATCTCTCGA 1194
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGluLysAsnIleTyrIleSer 660
 |||||
 Db 1193 ACCCTTACAGTTTCCATGATCACCTTACGGAATTCCTGGAGGGAACATCTATATTTCA 1134
 QY 661 ProLeuLysSerProTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro 680
 |||||
 Db 1133 CCCCTGAAGAGTCAATATAAATTTAGAGAGGTCTGCCAACAACCAAAATATGACTCA 1074

Alignment Scores:			
Pred. No.:	0	Length:	3232
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0
US-09-026-459A-37 (1-781) x US-08-470-091-1 (1-3232)			
QY	1 MetSerArgLeuLeuLysLysTyAspValLeuPheAlaLeuPheSerLysLeuGluArg	20	
Db	124 ATGTCAAGACTGTGTGAAGAGATGATGATGTTGTGTGACCTTCTACCAAAATGGGAAAAG	183	
QY	21 ThrCysGluLeuLeuIleTyLeuThrGlnProSerSerSerLysThrGluLeuAsnSer	40	
Db	184 ACATGTGAACCTTATATATTTGACACAAACCGACAGTGTGATCTACGAAATTAATCTT	243	
QY	41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln	60	
Db	244 GCAATGGTCTTAAAGAGTTTCTGGATCACATTTTATTAAGCTAAAGGGGAAATTAACAA	303	
QY	61 MetGlnAspAspLeuValLysSerPheGlnLeuMetLeuCysValLeuAspTyPheIle	80	
Db	304 ATGGAAGATGATCTGTGATTTCTATTCAGTTAATGATATGTCCTTGACTATTTTAT	363	
QY	81 LysLeuSerProProMetLeuLeuLysGluProTyLysTrpAlaValLysProIleAsn	100	
Db	364 AAACCTTCACTCCCTGATGTGTCTGAAGAACCAATTAACAGCTGTATTAACCATTAAT	423	
QY	101 GlySerProArgTrpProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu	120	
Db	424 GGTTCACCTCGAAGACCCAGCGAGTCGAGAACAGAGATCGACGATACGAAACAACTA	483	
QY	121 GlnAsnAspTrpArgIleIleGlnValLeuCysGlyGlnHisGluCysAsnIleAspGlu	140	
Db	484 GAAATGATACAAAGATTTATTGAAAGTTCTGTGAAGAACATGAATGATTAATATGATGAG	543	
QY	141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr	160	
Db	544 GTGAAAAAGTTTATTTCAAAAAATTTATTAACCTTTATGAATCTCTGTGACCTTGACAA	603	
QY	161 SerAsnGlyLeuProGluValGlnAsnLeuSerLysArgTyArgGluIleTyLeuLys	180	
Db	604 TCTAAATGACTTCCAGAGGTTGAAAAATCTTTCTTCAAAACGATACGAAGAAATTTATCTTAA	663	
QY	181 AsnLysAspLeuAspAlaArgLeuPheLeuAsnPheLysAspLysTrpLeuGlnThrAspSer	200	
Db	664 AATTAAGATCTGAGTACGAAAGATTAATTTTGTGATCATGATTAACACTCTTCAGACTGATTC	723	
QY	201 LAspSerPheGluThrGlnArgTrpProArgLysSerAsnLeuAspGluGluValAsn	220	
Db	724 ATGGAACGTTTGGAAACACAGAGAACCCAGCAAAAAGTAACCTTGATGAAAGAGTGAAAT	783	
QY	221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet	240	
Db	784 GTAAATTCCTCCACACACTCCAGCTTAGAGCTGTATGAACACTATACCAATTAATGAATG	843	
QY	241 LLeuAsnSerLysAspArgGlnProSerGlnAsnLeuLysSerTyPheAsnAsnCys	260	
Db	844 ATTTTAATTCAGCAAGATGATCAACCTTCGAAAATCTGATTTCTCTATTTTAACCACTGC	903	
QY	261 ThrValAsnProLysGluSerLysLeuLysValGlyValLysAspIleGlyTyrrIlePheLys	280	
Db	904 ACAGTAAATCCAAAAGAAAGATATCTGAAAAGAGTGAAGGATATAGGATACATCTTTAA	963	
QY	281 GlnLysPheAlaLysAlaValGlnGlnLysCysValGlnIleGlySerGlnArgTyLys	300	
Db	964 GAAATTTTCCTAAACCTGTGGGACAGGGTGTGTCTGAAAATTTGGATCACAGCATTAACA	1022	
QY	301 LeuGlyValArgLeuTyrrTyrrArgValMetGluSerMetLeuLysSerGluGluGluArg	320	

Db 1024 CTGGAGTTCGCTGTATATACCGAGTAATGAAATCCATGCTTAATTCAGAGAAAGAACGA 1083
 QY LeuSer11eGlnAsnPhseSerLeuLeuAsnAspAsn11ePheH1sMetSerLeuLeu 340
 Db 1084 TTATCCATTCAGAAATTTTACCAACCTTCGATGACACATTTTTCATATGCTTTATG 1143
 QY 341 AlaGysAlaLeuGluValValMetLeuThySerArgSerThySerGlnAsnLeuAsp 360
 Db 1144 GCGTGGCTCTTGAGGTGTATATGCGCATATGACATGACATGACATGACATGACAT 1203
 QY 361 SerGlyThrAspLeuSerPheProTrp11eLeuAsnVal11eAsnLeuLysAlaPheAsp 380
 Db 1204 TCTGGAAACAGATTTCTCTTCCATGATTCGAAATGCTTAATTTAAAGCCCTTGAT 1263
 QY 381 PheTyLysVal11eGlnSerPhe11eLysAlaGlu1YasnLeuThyArgGluMet11e 400
 Db 1264 TTTTACAAAGTCATGCAAGTTTATACAAAGCAAGACGACTTGACAAAGAAATGATA 1323
 QY 401 LysH1sLeuGluArgGysGluH1sArg11eMetGluSerLeuAlaTrpLeuSerAspSer 420
 Db 1324 AAACATTTTGAACGATGTGAACATGCAATGCAATCCCTTGCATGGCTCTCAGATTTCA 1383
 QY 421 ProLeuPheAspLeu11eLysGlnSerLysAspArgGluGlyProThyAspH1sLeuGlu 440
 Db 1384 CCTTATTTGATCTTATTAACAATCAAAAGACCGAAGACCAACTGATCACCCTTGAA 1443
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnH1sThyAlaAlaAspMetCysTrpLeu 460
 Db 1444 TCGCTGTGCTCTTAACTTCTCTCCAGATATATACACACGACGACATATATGATCTT 1503
 QY 461 SerProValArgSerProLysLysGlySerThyArgValAsnSerThyAlaAsn 480
 Db 1504 TCCCTCGTGAAGATCCCAAAAGAAAAAGGTCACTACCGCTAAATTCACGCAAAAT 1563
 QY 481 AlaGluThyGlnAlaThySerAlaPheGlnThyGlnLysProLeuLysSerThySerLeu 500
 Db 1564 GCAGAGACACAGCAACCTCAGCCTCCAGACCCAGACCAAGCATGTGAATCTACGCTCTT 1623
 QY 501 SerLeuPheTyLysLysVal1YtyrArgLeuAla1YtyrLeuArgLeuAsnThyLeuGysGlu 520
 Db 1624 TCCCTTTTATTAATAAAGTATATGCGTATGCGCTATGCGGCTAATATACATTTTGAAA 1683
 QY 521 ArgLeuLeuSerGlnH1sProGluLeuGlnH1s11eLeuTrpThyLeuPheGlnH1sThr 540
 Db 1684 CGCCTTCTGCTGAGCACCCAGAAATTAAGACATATCATCTGAGCCCTTTTCCAGACACC 1743
 QY 541 LeuGlnAsnGluTytyrGluLeuMetArgAspArgH1sLeuAspGln11eMetMetCysSer 560
 Db 1744 CTGCAGAAATGATGAACTCATGAGAGACAGGCAATTTGGACCAATTAATGATGTGTTCC 1803
 QY 561 MetTytyrGly11eCysLysVal1Yasn11eAspLeuLysPheLys11eLeuValThyAla 580
 Db 1804 ATGTATGSCATATGCAAGATGACAAATATGACCTTAATCAAAATCTGTAAACACA 1863
 QY 581 TytyrAspLeuProH1sAlaValGlnGluThyPheLysArgVal11eLysGlnGlu 600
 Db 1864 TACAAGAGATCTTCATGCTGTTGACAGACACATCAAAAGCTGTTTGTCAAAAGAAAG 1923
 QY 601 GluTytyrAspSer11eVal1PheTytyrAsnSerVal1PheMetGlnArgLeuLysThyAsn 620
 Db 1924 GAGTATGATCTTATATAGTATCTATATATGCGTCTTCATGAGAGACTGAAACAAAT 1983
 QY 621 11eLeuGlnTytyrAlaSerThyArgProProThyLeuSerPro11eProH1s11eProArg 640
 Db 1984 ATTTTGCATATGCTTCCACAGGCCCCCTTGTGCACCAATATCCATACCTTCTCTGA 2043
 QY 641 SerProTytyrAspPheProSerSerProLeuArg11eProGlyGlyYasn11eTytyrLieser 660
 Db 2044 AGCCCTTACAAAGTTTCCAGATCCCTTACGAGATTCCTGAGAGCAACATCTATATTCCA 2103
 QY 661 ProLeuLysSerProTytyrLys11eSerGluGlyLeuMetProThyProThyLysMetThyPro 680
 Db 2104 CCCTTAAGATGCCATATTAATTTCAAGAGTCTGCAACACCAACAAATATGCTCCA 2163

QY 681 ArgSerArg11eLeuValSer11eGlyGluSerPheGlyThySerGluLysPheGlnLys 700
 Db 2164 AGATCAAGAAATCTGTGATATCAATTTGGAATCAATCGGAGCTTCTGAGAGTCCAGAAA 2223
 QY 701 11eAsnGluMetValCysAsnSerAspArgVal11eLysAsnSerArg11eGlyGlySerAsn 720
 Db 2224 ATTAATCAATATGATATGATACAGCGACCGTGTCTCAAAAGAGTGTCTGAGAGAGAG 2283
 QY 721 ProProLysProLeuLysLysLeuArgPheAsp11eGluGlySerAspGluAlaAspGly 740
 Db 2284 CCGCTTAACCACTGAAAAAACTACGCTTGAATTTGAAGATGACAGATGACAGATGGA 2343
 QY 741 SerLysH1sLeuProGlyGlySerLysPheGlnGlnLysLeuAlaGluMetThySerThy 760
 Db 2344 AGTAAACATCTCCAGAGAGAGTCCAAATTTTCAGACAGAACTGGCAAAATGACTTACT 2403
 QY 761 ArgThyArgMetGlnLysGlnLysMetLysAspSerMetAspThySerAsnLysGluGlu 780
 Db 2404 CGAACCGAATGCAGAAACGAGAAATGAAATGATGATGATGATGATGATGATGATGATG 2463
 QY 781 Lys 781
 Db 2464 AAA 2466
 RESULT 9
 US-08-470-091-2/c
 Sequence 2, Application US/08470091
 Patent No. 5912236
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong-Ji
 APPLICANT: Hu, Shi-Xue
 APPLICANT: Benedict, William F.
 TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
 TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,091
 FILING DATE: JUN-16-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/038,760
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Poissant, Brian M
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 7409-025-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8664
 TELEFAX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3232 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: DNA
 US-08-470-091-2
 Alignment Scores:


```

|||||
Db 1073 AGATCAAGATCTGTATGATCAATGTTGGACTTGTGAAGTCCAGAAA 1014
OY 701 ILeasnglMetValCysasnSeraspArgValLeuLysArgSerAlaGluGlySerAsn 720
Db 1013 ATTAATCATATGTTATGTACAGCAGCCGTGTGCTCAAAAATAATGCTGAAGAGAGAAC 954
OY 721 ProProlYsProlLeuLysLysLeuArgPheaspIleGluGlySeraspGluAlaaspGly 740
Db 953 CCTCCTAAACCACTGAAAAAACTACGCTTGTATGTGAAGATCAAGATGAAGCAGATGGA 894
OY 741 SerLysHisLeuProGluYsLeuSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
Db 893 AGTAACATCTCCAGAGAGAGTCCAAATTTCCAGCAGAAACTGGCAAAATGACTTCTACT 834
OY 761 ArgThrArgMetGlnLysGlnLysMetLysaspSerMetLaspThrSeraspLysGlu 780
Db 833 CGAACACGATGCAAAAGCAGAAATGAATGATATGATGATACCTCAACACAGAGAGAG 774
OY 781 Lys 781
|||
773 AAA 771

```

```

RESULT 10
PCT-US94-10357-1
: Sequence 1, Application PC/TUS9410357
: GENERAL INFORMATION:
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
: TITLE OF INVENTION: Susceptibility Gene Product
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/10357
: FILING DATE: 13-SEP-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/121,108
: FILING DATE: 13-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: FP-UC 1117
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2994 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 139..2923
: PCT-US94-10357-1

```

```

Alignment Scores:
Pred. No.: 0
Score: 4014.00
Percent Similarity: 100.00%
Length: 2994
Matches: 780
Conservative: 1

```

```

Best Local Similarity: 99.878
Query Match: 99.93%
DB: 5
Gaps: 0
Mismatches: 0
Indels: 0
US-09-026-459a-37 (1-781) x PCT-US94-10357-1 (1-2994)
OY 1 MetSerArgLeuLeuLysLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
Db 580 ATGTCAAGACTGTTGAAGAAGTATGATGATGTTGTCACCTTTGAGCAAAATTTGGAAAAG 639
OY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerIleSerThrGluIleAsnSer 40
Db 640 ACATGTGACTATATATTTTGACACCAACCCAGAGTGCATATCTACAGATAATAATCT 699
OY 41 AlaLeuValLeuLysValSerTrrPleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
Db 700 GCATTGGCTGCTAAAGTTCTTGATCCATCTTTATTTATGCTAAAGGGGGAAGTATTACAA 759
OY 61 MetGlnaspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db 760 ATGGAAGATGATCTGGTGAATTCATTTCATTCAGTAACTGATGCTGCTGACTATTTAT 819
OY 81 LysLeuSerProProlMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db 820 AAACCTCCACCTCCCATGTTGCTCAAGAAACCATATATAACGCTGTTATACCCATTAT 879
OY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db 880 GGTTCACCTCGAACCAGCCAGCGGATCGAAGACAGAGATGCGAGATGCAAAACAACTA 939
OY 121 GlnAsnAspThrArgIleIleGluValLeuCysLysGlnHisGluCysAsnIleAspGlu 140
Db 940 GAAATGATACCAAGAAATATGAAAGTCTCTGTAAGAAACAAAGAAATGAATATGATAG 999
OY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetLysSerLeuGlyLeuValThr 160
Db 1000 GTGAAAATGTTTATTTCCAAATTTTATACCTTTATATGAAATTCCTTGACTGTAA 1039
OY 161 SerAsnGlyLeuProGluValGlnAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
Db 1060 TCTATATGACTTCCAGAGAGTGTGAAGAACTTTCTAAACGATAGGAAGAAATTTATCTTAA 1119
OY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 1120 AATAAAGATCTAGATGCAAGATTTATTTTGATCATGATTAACCTTCAGACTATATCT 1179
OY 201 IleaspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db 1180 ATAGACAGTTTTTGAACACAGACAGACACACGAAAGATTAACCTTGATGAAAGCTGAAT 1239
OY 221 ValIleProProlIleThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db 1240 GTAATTCCTCCACACACTCCAGTTAGACCTGTATATACACATTCACACATTAATGATG 1299
OY 241 IleuAsnSerAlaSeraspGlnProSerGlnAsnLeuIleSerTyrPheAsnAsnCys 260
Db 1300 ATTTTAATTCAGCAGATGATCAACCTTCAGAAATCTATTTCTATTTTAAACACGC 1359
OY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db 1360 ACAGTGAATCCAAAGAAAGATATATCTAAAGGATGAAGATATAGATACATCTTTTAA 1419
OY 281 GlnLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db 1420 GAGAAATTTGCTAAAGCTGTGGCAGAGGTTGTGTGAATTTGATACAGCATACAAA 1479
OY 301 LeuGlyValArgLeuTyrTyrArgValMetGlnSerMetLeuLysSerGluGlnGluArg 320
Db 1480 CTGGAGTTCCTTGTATTTACCGAGTATATGAAATCCATGCTTAAATCAGAAAGAGCA 1539
OY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1540 TTATCCATTCAAAATTTTACCAAACTTGTGAATGACACATTTTTCATATGCTTATTTG 1599

```

QY 341 AlaCysAlaLeuGluValIValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuasp 360
 |||||
 Db 1600 GCGTCCGCTCTTGAGGTGGTATGACCATATAGCAGAAAGTCAATCTAGAAATCTTGAT 1659
 QY 361 SerGlyThrAspLeuSerPheProTPIIleLeuAsnValIleuAsnLeuLysAlaPheasp 380
 |||||
 Db 1660 TCTGGAAACAGATTTGCTCTTCCATGATTCGAAATGCTTAAATTAACCCCTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
 |||||
 Db 1720 TTTTACAAAGATGATCGAAAGTTTATTCAAAGCAGAAAGCACTTGACAGAAATGATA 1779
 QY 401 LysHisLeuGluValArgCysGluHisArgIleMetGluSerLeuAlaTPIleuSerAspser 420
 |||||
 Db 1780 AAMCATTTTGAACATGTGAAACATCGAATCATGGAATCCCTTGACAGCTCTCAATTC 1839
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 |||||
 Db 1840 CTTTATTTGATCTTATTAACAATCAAGACCGAAGACCAACATGATCCTTGAA 1899
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
 |||||
 Db 1900 TCTGCTTCTCCCTTAATCTTCCCTCCAGAAATCAACACACGACAGATATGATCTT 1959
 QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
 |||||
 Db 1960 TCTCTCTGAATCTCCAAAGAAAAAGTTCAACTACCGGTCAATTCATCTGCAAT 2019
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 |||||
 Db 2020 CGAGAGACAAAGCAACCTCCAGCTCCAGACCAAGCAATGAAATCACTCTCTT 2079
 QY 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuLysGlu 520
 |||||
 Db 2080 TCACGTTTAAAAAAGTATCGGCTAGCCTATCTCGGCTAAATACATTTTGTA 2139
 QY 521 ArgLeuLeuSerGluHisProGluLeuGlnHisIleIleTPIleuPheGlnHisThr 540
 |||||
 Db 2140 CGCCTCTGCTGAGCACCAAGAAATAGAACATATCATCTGACCCTTTCCAGCACACC 2199
 QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetLeuTyrSer 560
 |||||
 Db 2200 CTGCGAATGAGTATGAACTCATGAGAGACAGCATTTGGACCAATTTGATGCTGCC 2259
 QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
 |||||
 Db 2260 ATGTATGGCATATGCAAGTCAAGAAATATGACCTTAATTCAAAATCATTTTACACACA 2319
 QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
 |||||
 Db 2320 TACAAAGATCTCTCTCATGCTGTTCAAGAGACATTCAAACGCTTTTGTGTAAGAAGAG 2379
 QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 |||||
 Db 2380 GAGTATGATTTCTATTATAGATATCTATTAACCTCGCTCATGAGACAGATGAAACAAAT 2439
 QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 |||||
 Db 2440 ATTTTGGATGCTGCTCCACAGGCCCTTACTTGTCCACATACCTACTTCTCTGGA 2499
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 |||||
 Db 2500 AGCCCTTACAGTTCTCTAGTCAACCTTACGGATTCCTGAGGAAACATCTATATTTC 2559
 QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
 |||||
 Db 2560 CCCCTGAAGAGTCCATATAAATTTTCAGAAAGTCTGCCAACACAAACAAATGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
 |||||
 Db 2620 AGATCAAGAATCTTATGATATCAATTTGGTGAATATTCGGGACTTTCGAGAGATTCACAGAA 2679

QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
 |||||
 Db 2680 ATTAATCATGATGTATGTAACAGGACCGGTGCTCAAAAAGATGCTGTAAGAAACAAAC 2739
 QY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly 740
 |||||
 Db 2740 CTTCTTAAACCGATGAAAAAACAATGATGATGAAAGATCATGATGAAACAGATGGA 2799
 QY 741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 |||||
 Db 2800 AGTAAACATCTCCAGAGAGATCCAAATTCAGCAGAAACTGGCAGAAATGACTTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
 |||||
 Db 2860 CGAACAGAAATGCAAAACAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2919
 QY 781 Lys 781
 |||
 Db 2920 AAA 2922
 |||
 RESULT 11
 US-08-328-673A-7
 ; Sequence 7, Application US/08328673A
 ; Patent No. 6210939
 ; GENERAL INFORMATION:
 APPLICANT: Gregory, Richard J.
 Willis, Ken N.
 Maneval, Daniel C.
 TITLE OF INVENTION: Recombinant Adenoviral Vector and
 Methods of use
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/328,673A
 FILING DATE: 25-Oct-1994
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/142,669
 FILING DATE: 25-OCT-1993
 APPLICATION NUMBER: US 08/233,669
 FILING DATE: 26-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Timothy S.
 REGISTRATION NUMBER: 35,367
 REFERENCE/DOCKET NUMBER: 016930-000920US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2995 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 139..2925
 OTHER INFORMATION: /product= "RB"
 /note= "retinoblastoma tumor suppressor"
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-08-328-673A-7

Alignment Scores:

Pred. No.:	0	Length:	2995
Score:	4007.00	Matches:	780
Percent Similarity:	99.87%	Conservative:	0
Best Local Similarity:	99.87%	Mismatches:	1
Query Match:	99.75%	Indels:	0
DB:	4	Gaps:	0

US-09-026-459a-37 (1-781) x US-08-328-673a-7 (1-2995)

Oy 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
Db 580 ATGTCAAGACTGTTCAGAAAGTATGATGTTGTTCCACTTCACCAATTTGGAAGG 639

Oy 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerLysLeuPheGluLeuSer 40
Db 640 ACATGTGAACCTATATTTATTTGACACACCCAGAGTTCGATATCTGCAAAATTAATCT 699

Oy 41 AlaLeuValLeuLysValSerTyrPheLeuLeuAlaLysGlyGluValLeuGln 60
Db 700 GCATTTGTCCTAAAGTTCTTGTGATCACAATTTTATTAAGCTAAAGGGAAGATTACAA 759

Oy 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db 760 ATGGAAGATGATCTGTGATTTCAATTCAGTAAATGCTATGTCCTTGACTATTTTAT 819

Oy 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db 820 AAATCTCACCTCCCATGTCCTCAAGAAACATTAATAAAGCTGTTATATACCATTAAT 879

Oy 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
Db 880 GGTTCACTCGAACACCCAGCGAGTGCACAAAGAGATGACGAGATAGCAAAACACTA 939

Oy 121 GluAsnAspThrArgIleIleGluValLeuCysLysGlnHisGlyCysAsnIleAspGlu 140
Db 940 GAAATCATATCAAGAAATTAATGAACTCTCTGTAAGAAACATGATTAATATAGTAGAG 999

Oy 141 ValLysAsnValTyrPheLysAspPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db 1000 GTGAAAATGTTATTTATCAAAAATTTATACCTTTATATGAAATCTCTGACATGTGAACA 1059

Oy 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGlyGluIleTyrLeuLys 180
Db 1060 TCTAATGGAATCTCCAGAGGTGAAAACCTTCTAAACGATACGAAGAAATTTATCTTAA 1119

Oy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 1120 AATTAAGATCTAGATGCAAGATATATTTTGTGATCATGATAAACCTTCAGACTGATCT 1179

Oy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
Db 1180 ATAGACGTTTGGAAACACAGAGAACACACGAAAGAAAGTAACCTTGATGAAGAGTGAT 1239

Oy 221 ValIleProIleHisThrProValArgThrValMetAsnThrIleGlnHisLeuMetIle 240
Db 1240 GTATTTTTCACACACTCCAGCTTATGAGACTGTTATTAACATATCAACATTAATGATG 1299

Oy 241 IleLeuAsnSerLysSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
Db 1300 ATTTTAATTTACAGAGTATATCACTTCAGAAATCTATATTCCTATTTTAACAACCTC 1359

Oy 261 ThrValAsnProLysGluSerLysLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db 1360 ACAGTGAATCCAAAAGAAAGTATCTGTAAGAGTCAAGAGATATAGATATCACTTTTAA 1419

Oy 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db 1420 GAGAAATTTGCTTAAAGCTGTGGGACAGGTTGTGGAATATGATCAACGACATTCAAA 1479

Oy 301 LeuGlyValArgLeuTyrTyrArgValMetGlnSerMetLeuLysSerGluGluGluArg 320

Db 1480 CTTGGAGTTCGCTTCTATACCGAGTAATGGAATTCATGCTTAATACGAGAGAGACGA 1539

Oy 321 LeuSerIleGlnAsnProPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1540 TTTTCATTTCAAAAATTTTATGACCAAACTTCGATATGACCAATTTTATATATGTCTTTAT 1599

Oy 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db 1600 GCGTGCGCTTGTGAGTTGTATAGCCACATATAGCGAAGATGATCATCTCAGATCTGAT 1659

Oy 361 SerGlyThrAspLeuSerPheProTyrPheLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db 1660 TCTGGACAGATTTGCTTCTCCATGATGATGATGATGCTTAATTTAAACCTTTGAT 1719

Oy 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluValLeuThrArgGluMetIle 400
Db 1720 TTTTCAAAAAGTATCGAAGATTTTATCAAGACAGAGCAACTTGACAAAGAAATGATA 1779

Oy 401 LysHisLeuGluArgCysGlnHisArgIleMetGluSerLeuAlaThrLeuSerAspSer 420
Db 1780 AAACATTTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1839

Oy 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
Db 1840 CCTTATTTGATCTTAATTAACAATCAAGAGACCGAGAGACCAACTGATCAGCTTGA 1899

Oy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAspMetTyrLeu 460
Db 1900 TCTGCTGTGCTCTTATCTCTCTCCAGAAATATACACTCCACCAATATGATCTT 1959

Oy 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCCTGTAGATCTCCAAAGAAAAAGTTCACTACAGCGTGAATTTCTCTCAAT 2019

Oy 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGACACCAAGCACTCAGCTCCAGACCCAGAGACCATGAAATCTACTCTCT 2079

Oy 501 SerLeuPheTyrLysValTyrArgLeuAlaArgLeuArgLeuSerThrLeuGlyGlu 520
Db 2080 TCACTTTTATAAAAAGTATGCTGCGTACGCTTCTCCGGCTAATATCACTTTGTGA 2139

Oy 521 ArgLeuLeuSerGlnHisProGluLeuGluHisIleIleThrPheLeuPheHisThr 540
Db 2140 CGCTCTCTGTGAGCACCCAGAAATTAAGATATCATCTGAGACCTTTTCCAGCACAC 2199

Oy 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetLecCysSer 560
Db 2200 CTCACGAATGAGTATGAACTCATGAGAGACAGGCAATTTGGACCAATATGATGTGTTCC 2259

Oy 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValAlaThrAla 580
Db 2260 ATGTATGCAATATGCAAGATGAAGAAATATAGACTTAATATCAAAATCATTTGTACACCA 2319

Oy 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
Db 2320 TACAAGATCTTCCTCAGCTGCTTCAAGAGACATCAAGCTGTTTGTATCAAGAGAGAG 2379

Oy 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db 2380 GATATGATCTCATATATATATATCTTAATCTGCTTCAAGAGACATGAAACAAAT 2439

Oy 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTTGAATATGCTTCCACAGGCCCCCTACCTTGTATACCAATACATCTCTCTGGA 2499

Oy 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysHisIleTyrIleSer 660
Db 2500 AGCCTTACAAATTTCTCAAGTACCCCTTACGAAATCTCTGAGGAGAACATCTATTTTCA 2559

Oy 661 ProLeuLysSerProTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro 680
Db 2560 CCGCTGAAGATGCATATTAATAATTTGAGAAAGCTGTGCCAACACCAACAAATAATGACTCCA 2619


```

1 CITY: Boston
2
3 STATE: MA
4
5 COUNTRY: USA
6
7 ZIP: 02109-2891
8
9 COMPUTER READABLE FORM:
10
11 MEDIUM TYPE: Floppy disk
12
13 MEDIUM TYPE: IBM PC compatible
14
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16
17 SOFTWARE: Patent In Release #1.0, Version #1.30
18
19 CURRENT APPLICATION DATA:
20
21 APPLICATION NUMBER: US/08/152,721B
22
23 FILING DATE: 15-Nov-1993
24
25 CLASSIFICATION: 435
26
27 ATTORNEY/AGENT INFORMATION:
28
29 NAME: Pasternack Esq., Sam
30
31 REGISTRATION NUMBER: 29,576
32
33 REFERENCE/DOCKET NUMBER: 181411-011DIV
34
35 TELECOMMUNICATION INFORMATION:
36
37 TELEPHONE: (617) 248-5000
38
39 TELEFAX: (617) 248-4000
40
41 INFORMATION FOR SEQ. ID NO.: 1:
42
43 SEQUENCE CHARACTERISTICS:
44
45 LENGTH: 2808 base pairs
46
47 TYPE: nucleic acid
48
49 STRANDEDNESS: both
50
51 TOPOLOGY: linear
52
53 MOLECULE TYPE: cDNA
54
55 HYPOTHETICAL: NO
56
57 ANTI-SENSE: NO
58
59 IMMEDIATE SOURCE:
60
61 CLONE: cDNA encoding p107
62
63 US-08-152-721B-1

```


Best Local Similarity: 24.21% Mismatches: 305
 Query Match: 18.16% Indels: 337
 DB: 1 Gaps: 32

US-09-026-459a-37 (1-781) x US-08-832-883-1 (1-4853)

QY 3 ArgLeuLeuLysLysIleuValLeuPheLeuSerLysLeuGluArgThrCys 22
 |||||
 DB 520 AGATTGAGAAAGAACTTCACTGCTGCTGTAATTTTAAAGAAATATGAAACCATTTT 579

QY 23 GluLeuIleuLysLeu-----ThrGlnProSerSerIleSerThrGlu-- 37
 |||||
 DB 580 CAGGACATCTTAAATACCTCAAGAGAGACACCTGTCAGACGAGGAGGAAACAG 639

QY 38 -----IleAsnSerAlaLeuValLeuLysValSerThrPheLeuLeu 53
 |||||
 DB 640 CGGCGACACCCCTGCTACTGCTGTAATTTTCCATTTTGTGGGCTTTTATATATAT 699

QY 54 AlaLysGluGluValLeuGlnMetGluAspLeuValIleSerPheGlnLeuMetLeu 73
 |||||
 DB 700 GCAAAAGGTATTTCCCATGATTAAGTATGATTTGTCATTAATTCACCTGCTGCTG 759

QY 74 CysValLeuAspIlePheIleLysLeuSerProMetLeuLysGluProTyrLys 93
 |||||
 DB 760 TGTGCTTGGACTTATGTT-----TATGGA 783

QY 94 ThrAlaValIleProIleAsnGly-----SerProArgThrProArgArgGly 109
 |||||
 DB 784 AATGACATCTGCTGCTCAATCGTAAGAACTTGTGAACCTTAATTTAAAGCTTATCT 843

QY 110 GlnAsnArgSerAlaArgIleAlaLysGlnLeuGlnAsnAspThrArgIleIleGluVal 129
 |||||
 DB 844 GAAGATTTTTCATGTAAGATTTCAACCTCTGCTGACCCCTGTAATCATTTGAGAAA 903

QY 130 LeuCysLysGluHisGluCysAsnIleAspGluValIleLysAsnVal-----TyrPhe 146
 |||||
 DB 904 CTGCTTCCTTACATGATGAGCTGCTGTTTGGAGCAAGGAGTAAAGAACATTTCTG 963

QY 147 LysAsnPheIleProPheMet-----AsnSer 155
 |||||
 DB 964 AAACCCATATATATGAGAAATTTATGAAAAAAGCTCCTTAAGGAAAAAGAAATCTTC 1023

QY 156 LeuGluLeuValThrSerAsnGlyLeuProGlu-----ValGlnAsnLeuSerLysArgTyr 174
 |||||
 DB 1024 ACTGGGTTTCTAGAACCTTGGAACTTGGAGAGAGTTTAAAGCCATCAATTAAGCCCTAT 1083

QY 175 GluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp--- 193
 |||||
 DB 1084 GAGGATATGTTTATCTGTTGGAAATTTAGATGAGCGGATATTTCTTGGAGAGATGCT 1143

QY 193 ----- 193

DB 1144 GAGGAGAAATTTGGACTCTCTCAAGGTCTGTAAGCCTGTTCAAGAACAGACTGCT 1203

QY 194 LysThrLeuGlnThrAspSerIle-----AspSerPheGluThrGlnArgThrProArg 211
 |||||
 DB 1204 GAAGGGGTGCGAAGAAATCTTACACAGCATTTTGACAAGTCCAAAGCATTTAGA 1263

QY 212 LysSerAsnLeuAspGluGluValAsnValIle-----ProProHisThrPro 227
 |||||
 DB 1264 ATCTCCACACCATTAACCTGCTTAGTACTTTAAGAGAAATAGCCCTTGTGAGCTCCA 1323

QY 228 ValArgThrValMetAsnThrIleGlnGlnLeuMetIleLeuAsnSerAlaSerAsp 247
 |||||
 DB 1324 GTTCTTACAGCTACGATACCTTGAAGTCTTACACACCATGCTGACAGGCTCAGAAAT 1383

QY 248 GlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSer 267
 |||||
 DB 1384 GCACCAAGTGAAGAAACAGATTCAGAGACATGTTCCAGAGATCCACAGGCT 1443

QY 268 IleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla-----Lys 285
 |||||
 DB 1444 ATGTGTAACAGACGTGAAGAAATGTTGAAATATATCTCAGCATTTCCAGCAAGACGAG 1503

QY 286 AlaValGluGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGluValArgLeu 305
 |||||
 DB 1504 GATTTCAAGTAAATTTGCTTAAAGAAATTTGCCAGCAAAATTTGCTTTTCCGAGATCTT 1563

QY 306 TyrTyrArgValMetGluSerMetLeuLysSerGlnGluLysLeuLeuSerIleGlnAsn 325
 |||||
 DB 1564 TACTTAAAGTATTAAGATCTGTTATTTGACAGAGCAAAAGAAAGACTAGGAGACATGAT 1623

QY 336 PheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGlu 345
 |||||
 DB 1624 TTATCTGGTATTTCTGGAACAAAGATGATTCACAGATCTCTTGGCGCTGCTTGAAG 1683

QY 346 ValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 365
 |||||
 DB 1684 GTGCTC-----ACTTTTCTTATTAAGCCCTCTGGGAT----- 1716

QY 366 SerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIle 385
 |||||
 DB 1717 ---TTTCCATTTATTTACTGAATATTTGATGCTGCTCTTATCATTTTATTAAGTGATA 1773

QY 386 GluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArg 405
 |||||
 DB 1774 GAAGTATTCATTAAGACAGAGAGATGCGCTTGTAGAGAGGTGGTAAACACTTAATCAG 1833

QY 406 CysGlnHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeu 425
 |||||
 DB 1834 ATTTGAAGAACAGATCTTAAGATCATTTGCTGAGAAACAGAGTCTCAGCTGGGAAAA 1893

QY 426 IleLysGlnSerLysAspArgGluGly-----ProThrAspHisLeu 439
 |||||
 DB 1894 ATTTGAGACAAATGAAGAAAGCTTCTTACATGTGAAGAGGTCAATGACCTCAGAAACCTG 1953

QY 440 GluSerAla-----CysProLeuAsnLeuProLeuGlnAsnAsnHis----- 453
 |||||
 DB 1954 GAAGGGAGATGAATTTGATTTGCTGCTGCTCCCTTGTAGCTCCAGAAAGGTGATGAA 2013

QY 454 -----ThrAlaAlaAsp 457
 |||||
 DB 2014 GTTCTGCTGATTAAGTGAAGACCTTGAAGAGCATTAACATCTCCAAACCATTTATGAT 2073

QY 458 MetTyrLeuSerProValArgSerProLysLys----- 469
 |||||
 DB 2074 AGGTACAGCTCCACAGCAGCAGCATACCAAGAGGGCTATTTGTGAGATGATAC 2133

QY 469 ----- 469

DB 2134 CCTCTGATGAGGAGGAGCGCTGGCGCATGCCCAACAGCCCTAGTCAATGCTGCCCT 2193

QY 470 -----GlySerThrThrArgValAsnSer----- 477
 |||||
 DB 2194 GTGCAGAAATGATATCTGGAGAGACTGTTCTCTGACACACAGTTCTCTGACAGACTTTGCTC 2253

QY 478 -----ThrAlaAsn----- 480
 |||||
 DB 2254 ACCATGGCAACCGCCACTGTACAGCCCAACATGAGGCAACGTAACCATTCCTGTGCAA 2313

QY 481 -----Ala 481
 |||||
 DB 481 GGTATTTGCCAATGAAATTTGAGGAGTAACTTCTCCCTGTCCTCAAGTCAATGTGGGGGG 2373

QY 482 GluThrGlnAla-----ThrSerAlaPheGln----- 490
 |||||
 DB 2374 CAGGACAAAGCTGTGACAGGCTCATCAGCCCTCAGTGTCTGAGCCCTGGCTGGAAT 2433

QY 490 ----- 490

DB 2434 CTGAGCTCTCAACAGGTGACAGAAACAATTTTGCATGCTCTGCTCAAGTGGCCATTCAA 2493

QY 491 -----ThrGln 492
 |||||
 DB 2494 CAGATTTCCCGAGGTGGCCAAAGCAGCAAGCAAGGCGCAGTCTGTAAACAGAGTATAT 2553

Tue Jan 21 10:03:26 2003

us-09-026-459a-37.rni

Page 25

Db	2908	AGAGGCCATGAAATTTCCTCCACAGAACTAAACAAAGATGAAACAGTAGAGAGATCGAT	2967
Qy	598	-----	598
Db	2968	CCAGTTATGAGTGCAAGAGACACCTTGCAGTTCACAGGCCACAGCTAGTTCCTCCACA	3027
Qy	599	-----GluGlnLutTyAspSerIleIle	606
Db	3028	CCTACTGGCCTCAGAGTGCACAGTGCACAGTGCACAGAAAGAGAGAGAGGGAGACCTCATTT	3087
Qy	607	ValPheTyrSerIleAlaPheMetGlnArgIleuLeuSerPheAspIleIleGlnIleTyr-----	624
Db	3088	CAGTTCACAAACAACATCTACATCAATAAACAGATTAAAGCATTTGCCATGAGTCTGCAGC	3147
Qy	625	AlaSerThrArgProPheThrIleuSerProIlePheProHisIleProArgSerProTyrLys	644
Db	3148	CGAAATATGAGATCTCTCTCCACCTCTCTCCCTATTCATTGTATGAAG-----	3192
Qy	645	PheProSerSerProLeuAspIle-----ProGlyLysIleTyrIleSerPro	661
Db	3193	----AAGGCTCTCCCTCGCGCAATACAGATTCTCCAAATCATCTCTCTACATTTGCCA	3249
Qy	662	IleuYsSerProTyrIleSerGluGlyLeuProThrProPheIleSerIleMetThrProArg	681
Db	3250	CATTAAATAT-----GAAACAATGCTTCTCTCTCGA	3279
Qy	682	SerArgIleLeuValSerIleGlyIleuSerPheGlyHisSerIleuLysPheGlnLysIle	701
Db	3280	GAAGAAATTTTCTTCAATCTACTCCAGCACAGT-----CCTTCAAAAGAGCATGAGGAATTT	3333
Qy	702	AsnGlnMetValLysAsnSerPheArgValLeuIleArgSerIleArgIleuLysSerAsnPro	721
Db	3334	AAATCAATATGATTA-----GCACTACAGAGAAA-----	3357
Qy	722	ProLysProLeuLysIleLysLeuArgPheAspIleGluLysIleSerAspLysIleAspLysSer	741
Db	3358	---ACTGCTACTAAAGAAAGAGAGAAATCTTTTGAGAGATGGAAGTGAATATACCTGCGAAA	3414
Qy	742	LysHisIleuPro-----GlyLysLysPheGlnGlnLysLeuIleAspIleMetThrSerThr	760
Db	3415	AGAAATTTGCCAGAAATATCATCTTGCCTTAATACCGCGCTCTCCAAAGATATGCTAATGAC	3474
Qy	761	Arg	761
Db	3475	CGT	3477

Search completed: January 19, 2003, 05:26:11
Job time : 114.428 secs

1
2
3

1
2
3

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 15:20:22 (Search time 63.8803 Seconds
(without alignments)
14944.909 Million cell updates/sec

Title: US-09-026-459A-36

Perfect score: 3113
Sequence: 1 GCGCGCATGTCAGACGCTGT.....AAATGAGATTTATGATAGT 3113

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents_NA:*
2: /cgn2_6/ptodata/1/jna/5A.COMB.seq:*
3: /cgn2_6/ptodata/1/jna/5B.COMB.seq:*
4: /cgn2_6/ptodata/1/jna/6A.COMB.seq:*
5: /cgn2_6/ptodata/1/jna/6B.COMB.seq:*
6: /cgn2_6/ptodata/1/jna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3105.4	99.8	3232	1	US-08-038-760-1
2	3105.4	99.8	3232	1	US-08-038-760-2
3	3105.4	99.8	3232	2	US-08-470-091-1
4	3105.4	99.8	3232	2	US-08-470-091-2
5	3105.4	99.8	3232	1	US-08-204-329-2
6	2415	77.6	2994	1	US-08-482-627-4
7	2415	77.6	2994	3	US-08-801-092-3
8	2415	77.6	2994	4	US-09-315-113-3
9	2413.4	77.5	2994	5	PCT-US94-10357-1
10	2412	77.5	2995	4	US-08-959-638-7
11	2410.4	77.4	2995	4	US-08-328-673A-7
12	68.8	2.2	2808	1	US-07-708-962-1
13	68.2	2.2	3249	1	US-08-106-493A-1
14	68.2	2.2	3249	1	US-08-429-264-1
15	68.2	2.2	4853	1	US-08-832-883-1
16	68.2	2.2	4853	2	US-08-832-877-1
17	65.6	2.1	2808	1	US-08-152-721B-1
18	59	1.9	7218	2	US-08-232-463-14
19	51	1.6	3747	4	US-09-213-293D-2
20	44.6	1.4	1803	4	US-09-134-001C-799
21	44.6	1.4	15363	4	US-08-961-527-139
22	44.4	1.4	20674	4	US-09-641-638-651
23	44	1.4	19124	2	US-08-487-826B-13
24	43.8	1.4	1056	4	US-09-134-001C-1550
25	43.2	1.4	509	4	US-09-030-607-202
26	43.2	1.4	509	4	US-09-605-785-202
27	43.2	1.4	509	4	US-09-439-313-202

28	43.2	1.4	509	4	US-09-352-616A-202	Sequence 202, App
29	43.2	1.4	509	4	US-09-232-149A-202	Sequence 202, App
30	43	1.4	5852	1	US-07-867-106-2	Sequence 2, Appl1
31	42.8	1.4	615	4	US-08-998-416-186	Sequence 186, App
32	42.6	1.4	1189	1	US-08-307-581-2	Sequence 2, Appl1
33	42.6	1.4	2606	4	US-09-234-827B-3	Sequence 3, Appl1
34	42.4	1.4	1186	2	US-08-731-722-5	Sequence 5, Appl1
35	42	1.3	665	2	US-08-883-795A-36	Sequence 36, Appl1
36	42	1.3	1864	4	US-09-468-265-4	Sequence 4, Appl1
37	41.8	1.3	1679	4	US-09-306-060-1	Sequence 1, Appl1
38	41.4	1.3	19124	2	US-08-487-826B-13	Sequence 13, Appl1
39	41.2	1.3	821	4	US-08-998-416-541	Sequence 541, App
40	41.2	1.3	837	4	US-08-998-416-288	Sequence 288, App
41	41.2	1.3	2030	2	US-08-705-937-7	Sequence 7, Appl1
42	40.6	1.3	860	4	US-08-998-416-287	Sequence 287, App
43	40.6	1.3	4078	2	US-08-960-022-3	Sequence 3, Appl1
44	40.6	1.3	6265	4	US-09-129-112-3	Sequence 3, Appl1
45	40.6	1.3	12124	1	US-08-181-271A-36	Sequence 36, Appl1

ALIGNMENTS

RESULT 1
US-08-038-760-1
Sequence 1, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
NUMBER OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,760
FILING DATE: 19930325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1
Query Match 99.8%; Score 3105.4; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	7	ATGCAAGACGTGTGAAACAAAGTATGAGATGTGGTTTGGACGTCTACACAAATTGGAAAG	66
Db	124	ATGCAAGACGTGTGAAABAAAGATGATGATGATATGTTTGGACGTCTACAGAAATTGGAAAG	183
OY	67	ACATGTGAACCTTATATATTTGACACAACCCAGCAGTTGCGATATCTACTGAAATAAATTCG	126
Db	184	ACATGTGAACCTTATATATTTGACACAACCCAGAGAGTTGCGATATCTACTGAAATAAATTCG	243
OY	127	GCAATTGGTCTTAAAGTTTCTTGATACACTTTTATAGCTAAAGGGAAGATATACAA	186
Db	244	GCAATTGGTCTTAAAGTTTCTTGATACACTTTTATAGCTAAAGGGAAGATATACAA	303
OY	187	ATGGAAGATGATCTGTGATTTTCATTTCAGTTATAGCTATGTGTCTTGACTATTTTAT	246
Db	304	ATGGAAGATGATCTGTGATTTTCATTTCAGTTATAGCTATGTGTCTTGACTATTTTAT	363
OY	247	AAACCTGCACCTCCCATCTGCTCAAGAAACATATATAAAGCGTGTATATACCATTAT	306
Db	364	AAACCTGCACCTCCCATCTGCTCAAGAAACATATATAAAGCGTGTATATACCATTAT	423
OY	307	GGTTTCACCTGGAACCCAGGCGGTCGGAACAGAGAGGACAGATATAGCAAAACAAC	366
Db	424	GGTTTCACCTGGAACCCAGGCGGTCGGAACAGAGATGCAAGATATAGCAAAACAAC	483
OY	367	GAAATGATACAAAGATTTATGAATCTCTGTGAAGAACTGAATGTATATAGTAGAG	426
Db	484	GAAATGATACAAAGATTTATGAATCTCTGTGAAGAACTGAATGTATATAGTAGAG	543
OY	427	GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATCTCTGTGACCTGTGACA	486
Db	544	GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATCTCTGTGACCTGTGACA	603
OY	487	TCTATAGGACCTTCGAGAGGTTGAAATCTTCTTAAACGATTCGAAAGAAATTTTCTTAA	546
Db	604	TCTATAGGACCTTCGAGAGGTTGAAATCTTCTTAAACGATTCGAAAGAAATTTTCTTAA	663
OY	547	AATTAAGATCTAGATGCAAGATTTATTTTGGATCATGATATAACCTCTTCACACTGATCT	606
Db	664	AATTAAGATCTAGATGCAAGATTTATTTTGGATCATGATATAACCTCTTCACACTGATCT	723
OY	607	ATAGACAGTTTGAACACACAGAACACACACGAAAAAGTAACCTTGATGTAAGAGTGAT	666
Db	724	ATAGACAGTTTGAACACACAGAACACACGAAAAAGTAACCTTGATGTAAGAGTGAT	783
OY	667	GTAATTCCTCCACACACCTCCAGTTAGAGACTGTATGAACACTATCCAAACTTATATGAT	726
Db	784	GTAATTCCTCCACACACCTCCAGTTAGAGACTGTATGAACACTATCCAAACTTATATGAT	843
OY	727	ATTTTAAATTCAGCAAGTATCAACCTTCAGAAAACTGATTTTCTATTTTAAACAACCTGC	786
Db	844	ATTTTAAATTCAGCAAGTATCAACCTTCAGAAAACTGATTTTCTATTTTAAACAACCTGC	903
OY	787	ACAGTAATTCGAAAAAGAAATATCTGTATATAAAGGTGAAGAAATATAGATATCACTTTTAA	846
Db	904	ACAGTAATTCGAAAAAGAAATATCTGTATATAAAGGTGAAGAAATATAGATATCACTTTTAA	963
OY	847	GAGAAATTTGCTAAAGCTGTGTGGACACAGGGTGTGTCTGAAATTTGGATCACAGCATTCAAA	906
Db	964	GAGAAATTTGCTAAAGCTGTGTGGACACAGGGTGTGTCTGAAATTTGGATCACAGCATTCAAA	1023
OY	907	CTTGGAGTTCGCTGTATTTACCGAGTATATGGAATCCATGCTTAAATCAGAAAGAAACGA	966
Db	1024	CTTGGAGTTCGCTGTATTTACCGAGTATATGGAATCCATGCTTAAATCAGAAAGAAACGA	1083
OY	967	TTTATTCATTCGAAATTTTATAGCAACCTTGATGACAACTTTTTCATATGTCTTATATG	1026
Db	1084	TTTATTCATTCGAAATTTTATAGCAACCTTGATGACAACTTTTTCATATGTCTTATATG	1144
OY	1027	GCGTGCAGCTCTTGAGGTGTATATGGCCACATATAGCCAAAGATCATCTCGAAATCTTGAT	1086
Db	1144	GCGTGCAGCTCTTGAGGTGTATATGGCCACATATAGCCAAAGATCATCTCGAAATCTTGAT	1203

QY	1087	TCGTGGAAACGATTTGGCTTTCCTCCGACGATCTCGAATGCGCTTAATTTAAAGCCCTTGAT	1146
Db	1204	TCGTGGAAACGATTTGCTTCTCCCATGSAATTCGATATGTCCTTAATTTAAAGCCCTTGAT	1263
QY	1147	TTTTACAAAGTGATCGAAAGTTTATCAAGACGAAGGCACCTTGACAGAAGATGATA	1206
Db	1264	TTTTACAAAGTGATCGAAAGTTTATCAAGACGAAGGCACCTTGACAGAAGATGATA	1323
QY	1207	AAACATTATGAAACGATGTGAATCATCGAATCATGSAATCCCTTGATGGCTCGATATCA	1266
Db	1324	AAACATTATGAAACGATGTGAATCATCGAATCATGSAATCCCTTGATGGCTCGATATCA	1383
QY	1267	CCCTTATTTGATGCTTATTTAAACATCAAGGACCCGAAAGGCCAACTGATCATCTTGAA	1326
Db	1384	CCCTTATTTGATGCTTATTTAAACATCAAGGACCCGAAAGGCCAACTGATCATCTTGAA	1443
QY	1327	TCGTCTGTGCTCTTAATCTTATCTCTCTCCAGAAATATCACTGCGAGCAGATATGATCTT	1386
Db	1444	TCGTCTGTGCTCTTAATCTTATCTCTCTCCAGAAATATCACTGCGAGCAGATATGATCTT	1503
QY	1387	TCCTCCTTAAGATCTCCCAAAAAGGTTCTACCTACGCGGTGAATTTCTATGCGAAT	1446
Db	1504	TCCTCCTTAAGATCTCCCAAAAAGGTTCTACCTACGCGGTGAATTTCTATGCGAAT	1563
QY	1447	GCAGAGACACAAAGCACTCAAGCCTTCAGACCCGAGAACCATTTGAATATCTCCTCTT	1506
Db	1564	GCAGAGACACAAAGCACTCAAGCCTTCAGACCCGAGAACCATTTGAATATCTCCTCTT	1623
QY	1507	TCACGTGTTTTATAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA	1566
Db	1624	TCACGTGTTTTATAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA	1683
QY	1567	CGCCTCTGTGCTGAGACCCGCAAGTATTTGAACATCATCTGSAACCTTTTCAGCAACAC	1626
Db	1684	CGCCTCTGTGCTGAGACCCGCAAGTATTTGAACATCATCTGSAACCTTTTCAGCAACAC	1743
QY	1627	CTGCAGAATGAGTATGAACTCATAGAGACAGGCAATTTGGACCAATATGATGTGTTCC	1686
Db	1744	CTGCAGAATGAGTATGAACTCATAGAGACAGGCAATTTGGACCAATATGATGTGTTCC	1803
QY	1687	ATGATATGGCATATGCAAAAGTAAAGAAATATGACCTTAAATTCAAATCATTTGTAAACGA	1746
Db	1804	ATGATATGGCATATGCAAAAGTAAAGAAATATGACCTTAAATTCAAATCATTTGTAAACGA	1863
QY	1747	TACGAAGATCTCCGACAGCGTTCAGAGAACTTCAAAAGCTTTTGATCAAAAAGAG	1806
Db	1864	TACGAAGATCTCCGACAGCGTTCAGAGAACTTCAAAAGCTTTTGATCAAAAAGAG	1923
QY	1807	GAGTATGATTTATTAATATGATATTCATTAACCTCGCTTCATATGACAGACTGAAGAACAT	1866
Db	1924	GAGTATGATTTATTAATATGATATTCATTAACCTCGCTTCATATGACAGACTGAAGAACAT	1983
QY	1867	ATTTTGGAGTATGCTCCACAGAGGCCCTTCACTGTGTACACAAATACCTCATCTCTCGA	1926
Db	1984	ATTTTGGAGTATGCTCCACAGAGGCCCTTCACTGTGTACACAAATACCTCATCTCTCGA	2043
QY	1927	AGCCCTTACAAAGTTCCAAATGTCAACCTTACGATATCTCGAAGGAAACATCATATTTCA	1986
Db	2044	AGCCCTTACAAAGTTCCAAATGTCAACCTTACGATATCTCGAAGGAAACATCATATTTCA	2103
QY	1987	CCCCCTGAAGCTCCATTAATTAATTTTCAGAAAGTCTGCGACACACCACAAAAATGACTCA	2046
Db	2104	CCCCCTGAAGCTCCATTAATTAATTTTCAGAAAGTCTGCGACACACCACAAAAATGACTCA	2163
QY	2047	AGATCAAGAAATCTTGAATTCATATTTGGTGAATCAATTCGGAGCTCTGGAAGTTCAGAAA	2106
Db	2164	AGATCAAGAAATCTTGAATTCATATTTGGTGAATCAATTCGGAGCTCTGGAAGTTCAGAAA	2223
QY	2107	ATTAATTCAGTGTGATGTAAACAGGACCGCTGTCTCAAAAGAACTGCTGAAGAGCAAC	2166
Db	2224	ATTAATTCAGTGTGATGTAAACAGGACCGCTGTCTCAAAAGAACTGCTGAAGAGCAAC	2283
QY	2167	CCCTCTTAACCACTTAAAAAATCTACGCTTTGTGATTTGAAGATCAGATGCAAGCAGATGGA	2286

[illegible]

```

? TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
? NUMBER OF SEQUENCES: 3
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pennie & Edmonds
? STREET: 1155 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: U.S.A.
? ZIP: 10036-2711
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/038,760
? FILING DATE: 19930325
?
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Poissant, Brian M
? REGISTRATION NUMBER: 28,462
? REFERENCE/DOCKET NUMBER: 7409-025-999
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 790-9090
? TELEFAX: (212) 869-9741/8864
?
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3232 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: double
? TOPOLOGY: not relevant
?
? MOLECULE TYPE: DNA
?
? US-08-038-760-2
?
Query Match          99.8%; Score 3105.4; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0
?
QY 7 ATGTCAAGACTGTGGAAGAAGATGATGATGTTGTTGCACCTCTTCAGCAAAATTGGAAGG 66
Db 3113 ATGTCAAGACTGTGGAAGAAGATGATGATGTTGTTGCACCTCTTCAGCAAAATTGGAAGG 3054
?
QY 67 ACATGTCACTTATATATTGACACACACCACAGTTGATATCTACTGAAATTAATTC 126
Db 3053 ACATGTCACTTATATATTGACACACACCACAGTTGATATCTACTGAAATTAATTC 2594
?
QY 127 GCATGTGCTAAAGTTCTTCTTGATCACATTTTATTAGCTAAAGGGAAGTTCACAA 186
Db 2993 GCATGTGCTAAAGTTCTTCTTGATCACATTTTATTAGCTAAAGGGAAGTTCACAA 2934
?
QY 187 ATGGAAGATGATCGTGGTATTCATTTCAGTTAAATGCTATGTCCTTGACATATTTATT 246
Db 2933 ATGGAAGATGATCGTGGTATTCATTTCAGTTAAATGCTATGTCCTTGACATATTTATT 2874
?
QY 247 AAATCTCACTCCCAATGTCGTCAAGAACAATTAAGCAAGCTGTATACCCATTAT 306
Db 2873 AAATCTCACTCCCAATGTCGTCAAGAACAATTAAGCAAGCTGTATACCCATTAT 2814
?
QY 307 GGTTCACCTCGAACACCCAGGCGAGTCAAGACAGAGTGCACGAGTACGAAACAACTA 366
Db 2813 GGTTCACCTCGAACACCCAGGCGAGTCAAGACAGAGTGCACGAGTACGAAACAACTA 2754
?
QY 367 GAAATGATACAAAGATTAATGAAAGTCTCTGTAAGAAACAATGATTAATATGATGAG 426
Db 2753 GAAATGATACAAAGATTAATGAAAGTCTCTGTAAGAAACAATGATTAATATGATGAG 2694
?
QY 427 GTGAAAATGTTTATTCACAAAATTTTATACCTTTATACCTTTGAAATCTCTTGAAGTGTACA 486
Db 2693 GTGAAAATGTTTATTCACAAAATTTTATACCTTTATACCTTTGAAATCTCTTGAAGTGTACA 2634
?
QY 487 TCTATGACCTTCAGAGGTTGAAATCTTTTCAAAACGATACGAAGAATTTATCTTTAA 546
?

```

Db 2633 TCTATGACCTCCAGAGCTGGAAAATCTTCTTAACGATACGAGAAATTTATCTTAA 2574
QY 547 AATAAGATCTAGATGCAAGATTAATTTTGGATCATGATTAAGCTCTCAGACTGATTC 606
Db 2573 AATAAGATCTAGATGCAAGATTAATTTTGGATCATGATTAAGCTCTCAGACTGATTC 2514
QY 607 ATAGACAGTTTGAACACAGACAGAACACAGAAAAGTAACTTGAATGAGAGGTGAT 666
Db 2513 ATAGACAGTTTGAACACAGACAGAACACAGAAAAGTAACTTGAATGAGAGGTGAT 2454
QY 667 GTAAATCTCCACACACTCCAGTTAGACTGTATGAACTATTCACAACTTAATGATG 726
Db 2453 GTAAATCTCCACACACTCCAGTTAGACTGTATGAACTATTCACAACTTAATGATG 2394
QY 727 ATTTTAAATTCAGCAAGTATCAACTTTCAGAAAATCTGATTTTCTATTTTAACTG 786
Db 2393 ATTTTAAATTCAGCAAGTATCAACTTTCAGAAAATCTGATTTTCTATTTTAACTG 2334
QY 787 ACAGGATCCAAAAGAAAGTATCTGAAAAGATGAAAGTATAGATATCTTTAAA 846
Db 2333 ACAGGATCCAAAAGAAAGTATCTGAAAAGATGAAAGTATAGATATCTTTAAA 2274
QY 847 GAGAAATTTGCTAAAGCTTGAGGACAGAGTGTGTGCAAAATTTGATCAGACGATACAA 906
Db 2273 GAGAAATTTGCTAAAGCTTGAGGACAGAGTGTGTGTGCAAAATTTGATCAGACGATACAA 2214
QY 907 CTGAGAGTGGCTGTGTATTTACCGATATAGGAATTCATGCTTAAATCAGAAAGAACGA 966
Db 2213 CTGAGAGTGGCTGTGTATTTACCGATATAGGAATTCATGCTTAAATCAGAAAGAACGA 2154
QY 967 TTATCCATTCAAAATTTTAGCAAACTCTGAAATGACAACTTTTTCATATGCTTTATG 1026
Db 2153 TTATCCATTCAAAATTTTAGCAAACTCTGAAATGACAACTTTTTCATATGCTTTATG 2094
QY 1027 GCGTGGCTCTTGGAGTTGTAATGCGACATATAGCAAGATACATCTGAAATCTTGAT 1086
Db 2093 GCGTGGCTCTTGGAGTTGTAATGCGACATATAGCAAGATACATCTGAAATCTTGAT 2034
QY 1087 TCTGGACAGATTTGCTTCTTCCCATGATCTGAAATGCTTAAATTTAAAGCTTTGAT 1146
Db 2033 TCTGGACAGATTTGCTTCTTCCCATGATCTGAAATGCTTAAATTTAAAGCTTTGAT 1974
QY 1147 TTTTACAAGATGCAAAATTTTATCAAAAGCAAGAGCAACTGACAGAAAGATGAT 1206
Db 1973 TTTTACAAGATGCAAAATTTTATCAAAAGCAAGAGCAACTGACAGAAAGATGAT 1914
QY 1207 AAACATTTAGACGATGTGAACATCGAATCATGGAATCCCTGCAATGGCTCTCAGATTCA 1266
Db 1913 AAACATTTAGACGATGTGAACATCGAATCATGGAATCCCTGCAATGGCTCTCAGATTCA 1854
QY 1267 CCTTATTTGATCTTATTAACAATCAAAAGACCGAGAGGACCAACTGATCACTTGAA 1326
Db 1853 CCTTATTTGATCTTATTAACAATCAAAAGACCGAGAGGACCAACTGATCACTTGAA 1794
QY 1327 TCTGCTGTCTCTTAATCTTCTCTCCAGATTAATCAACCTGACAGAGATATGATCT 1386
Db 1793 TCTGCTGTCTCTTAATCTTCTCTCCAGATTAATCAACCTGACAGAGATATGATCT 1734
QY 1387 TCTGCTGTAAAGTCTCCAAAGAAAAGGTTCACTACGCGGTGTAATTTCTACTGCAAT 1446
Db 1733 TCTGCTGTAAAGTCTCCAAAGAAAAGGTTCACTACGCGGTGTAATTTCTACTGCAAT 1674
QY 1447 GCAGAGACAGCAAGCACTGAGCTTCAGAGACCCAGAGCAAGCAATGTAATCTACTCT 1506
Db 1673 GCAGAGACAGCAAGCACTGAGCTTCAGAGACCCAGAGCAAGCAATGTAATCTACTCT 1614
QY 1507 TCACTGTTTTTAAAAAAGTATCGGCTAGCCTATCTCGGCTAAATACACTTTGTGA 1566
Db 1613 TCACTGTTTTTAAAAAAGTATCGGCTAGCCTATCTCGGCTAAATACACTTTGTGA 1554
QY 1567 CGCCTTCTGTCTGAGACCCAGAAATTAAGACATATCATGTGACCCCTTTTCAGACAC 1626
Db 1553 CGCCTTCTGTCTGAGACCCAGAAATTAAGACATATCATGTGACCCCTTTTCAGACAC 1494

QY 1627 CTGACAGATGATATGAACATCATGAGACAGGCAATTTGGACCAATTAATGATGTCTCC 1686
Db 1493 CTGACAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1434
QY 1687 ATGTATGCAATATGCAAAAGTGAAGATATAGACCTTAAATTCAMAATCATTTGACAGCA 1746
Db 1433 ATGTATGCAATATGCAAAAGTGAAGATATAGACCTTAAATTCAMAATCATTTGACAGCA 1374
QY 1747 TACAGAGATCTTCCATGATGCTGTCAGAGACATTCAAACGCTGTTTGTATCAAGAAAG 1806
Db 1373 TACAGAGATCTTCCATGATGCTGTCAGAGACATTCAAACGCTGTTTGTATCAAGAAAG 1314
QY 1807 GAGTATGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1866
Db 1313 GAGTATGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1254
QY 1867 ATTTTCAGATGCTTCCACAGAGGCCCCCTACCTTGTACCAATACCTCATCTCTGA 1926
Db 1253 ATTTTCAGATGCTTCCACAGAGGCCCCCTACCTTGTACCAATACCTCATCTCTGA 1194
QY 1927 AGCCCTTACAGTTTCTGATGCTTACCCCTTACGATTCCTGAGAGGACATCTATTTTCA 1986
Db 1193 AGCCCTTACAGTTTCTGATGCTTACCCCTTACGATTCCTGAGAGGACATCTATTTTCA 1134
QY 1987 CCCCTGAGAGTCCATATTAATTTTCAAGAGTCTGCCAACCAACCAAAATGACTCCA 2046
Db 1133 CCCCTGAGAGTCCATATTAATTTTCAAGAGTCTGCCAACCAACCAAAATGACTCCA 1074
QY 2047 AGATCAAGATCTTATGATCAATTTGATGATCATCTGAGACTTCTGAGAACTTCAGAA 2106
Db 1073 AGATCAAGATCTTATGATCAATTTGATGATCATCTGAGACTTCTGAGAACTTCAGAA 1014
QY 2107 ATTAATCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2166
Db 1013 ATTAATCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 954
QY 2167 CCTCTTAAACCACTGAAAAAACTACGCTTTGATATTTGAAGATCAGATGAAGCAGATGA 2226
Db 953 CCTCTTAAACCACTGAAAAAACTACGCTTTGATATTTGAAGATCAGATGAAGCAGATGA 894
QY 2227 AGTAAACATCTCCAGAGAGTCCAAATTTTCAAGCAAACTGCGAAGATCACTTACT 2286
Db 893 AGTAAACATCTCCAGAGAGTCCAAATTTTCAAGCAAACTGCGAAGATCACTTACT 834
QY 2287 CGAACAGATGCAAAAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
Db 833 CGAACAGATGCAAAAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 774
QY 2347 AATGAGATCTCAGAGACTTGTGTGAGACATGTGTACACTCTGGAATCATTTGTCTCA 2406
Db 773 AATGAGATCTCAGAGACTTGTGTGAGACATGTGTACACTCTGGAATCATTTGTCTCA 714
QY 2407 CAGATGATGATTAATTAATTTTCCAGGTTCTGTTATGACCAATTAATATCTTCACT 2466
Db 713 CAGATGATGATTAATTAATTTTCCAGGTTCTGTTATGACCAATTAATATCTTCACT 654
QY 2467 CTTTGTGTGATTAATTAATTTTGAAGATGATGATGATGATGATGATGATGATGATGAT 2526
Db 653 CTTTGTGTGATTAATTAATTTTGAAGATGATGATGATGATGATGATGATGATGATGAT 594
QY 2527 ATGTATGATGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2586
Db 593 ATGTATGATGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 534
QY 2587 AGTTGATGATGATTTTCCCTTCCAAAGTAAATTTGCTGTTATGATGATGATGATGATGAT 2646
Db 533 AGTTGATGATGATTTTCCCTTCCAAAGTAAATTTGCTGTTATGATGATGATGATGATGAT 474
QY 2647 ATGGCCCTAGATGAGAGTCTGATTAACCCAGGCTGCTGATCACTGATGATGATGATGATGAT 2706
Db 473 ATGGCCCTAGATGAGAGTCTGATTAACCCAGGCTGCTGATCACTGATGATGATGATGATGAT 414

[illegible]

```

1      RESULT 3
2      US-08-470-091-1
3      : Sequence 1, Application US/08470091
4      : Patent No. 5912236
5      : GENERAL INFORMATION:
6      : APPLICANT: Xu, Hong-Ji
7      : APPLICANT: Hu, Shi-Xue
8      : TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
9      : TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
10     : NUMBER OF SEQUENCES: 3
11     : CORRESPONDENCE ADDRESS:
12     : ADDRESSEE: Pennie & Edmonds
13     : STREET: 1155 Avenue of the Americas
14     : CITY: New York
15     : STATE: New York
16     : COUNTRY: U.S.A.
17     : ZIP: 10036-2711
18     :
19     : COMPUTER READABLE FORM:
20     : MEDIUM TYPE: Floppy disk
21     : COMPUTER: IBM PC compatible
22     : OPERATING SYSTEM: PC-DOS/MS-DOS
23     : SOFTWARE: PatentIn Release #1.0, Version #1.25
24     : CURRENT APPLICATION DATA:
25     : APPLICATION NUMBER: US/08/470,091
26     : FILING DATE: JUN-16-1995
27     : CLASSIFICATION: 514
28     : PRIOR APPLICATION DATA:
29     : APPLICATION NUMBER: US/08/038,760
30     : FILING DATE:
31     : ATTORNEY/AGENT INFORMATION:
32     : NAME: Poissant, Brian M
33     : REGISTRATION NUMBER: 28,462
34     : REFERENCE/DOCKET NUMBER: 7409-025-999
35     : TELECOMMUNICATION INFORMATION:
36     : TELEPHONE: (212) 790-9090
37     : TELEFAX: (212) 869-9741/8864
38     : TELEFAX: 66141 PENNIE
39     : INFORMATION FOR SEQ ID NO: 1:
40     : SEQUENCE CHARACTERISTICS:
41     : LENGTH: 3232 base pairs
42     : TYPE: nucleic acid
43     : STRANDEDNESS: double
44     : TOPOLOGY: not relevant
45

```

```

? MOLECULE TYPE: DNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 19..2469
US-08-470-091-1

```

Query Match 99.8%; Score 3105.4; DB 2; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

0Y	7	ATGTCAAGCTGTGGAGAGAGTATGATGATGTTTCACTCTCAGCAAAATGGAAGG	66
Db	124	ATGTCAAGCTGTGGAGAGAGTATGATGATGTTTCACTCTCAGCAAAATGGAAGG	183
0Y	67	ACATGTGAACCTTATATATTTGACACACCCAGAGTTCGATATCTAGTAAGAAATATTC	126
Db	184	ACATGTGAACCTTATATATTTGACACACCCAGAGTTCGATATCTAGTAAGAAATATTC	243
0Y	127	GCATTGGTCTTAAAAGTTCTTGATCACATTTTATTAAGTCTAAAAGGAGATTCACA	186
Db	244	GCATTGGTCTTAAAAGTTCTTGATCACATTTTATTAAGTCTAAAAGGAGATTCACA	303
0Y	187	ATGGAAGATGATCTGTGATATTCATTTCAGTAAATGCTATGCTCCCTGACTATTTATTT	246
Db	304	ATGGAAGATGATCTGTGATATTCATTTCAGTAAATGCTATGCTCCCTGACTATTTATTT	363
0Y	247	AAACTGTACCCCATGTTGTGCTCAAGAACCATATTAACACGCTGTATATCCCATTAAT	306
Db	364	AAACTGTACCCCATGTTGTGCTCAAGAACCATATTAACACGCTGTATATCCCATTAAT	423
0Y	307	GGTTCACTCGAACCCAGGCGAGTCAAGACAGAGTGCACGATACCAAAACACTA	366
Db	424	GGTTCACTCGAACCCAGGCGAGTCAAGACAGAGTGCACGAGTACCAAAACACTA	483
0Y	367	GAAATGATACAGAAATTTATGTAAGTCTCTGTAAACAGCAATGAATTAATATAGATGAG	426
Db	484	GAAATGATACAGAAATTTATGTAAGTCTCTGTAAACAGCAATGAATTAATATAGATGAG	543
0Y	427	GTAAGAAATGTTTATTTCAAAATTTTATACCTTTTATGAATTCCTTGAGCTGTAAAC	486
Db	544	GTAAGAAATGTTTATTTCAAAATTTTATACCTTTTATGAATTCCTTGAGCTGTAAAC	603
0Y	487	TCTAATGACTTCAGAGGTTGAAAATCTTTCTTAACAGATACAGAAATTTATCTTAA	546
Db	604	TCTAATGACTTCAGAGGTTGAAAATCTTTCTTAACAGATACAGAAATTTATCTTAA	663
0Y	547	AATTAAGATCATAGATGACAGATTAATTTTGGATCATATTAACCTCTTCAGACTGATCT	606
Db	664	AATTAAGATCATAGATGACAGATTAATTTTGGATCATATTAACCTCTTCAGACTGATCT	723
0Y	607	ATTGACAGTTTTGAAACACAGACAGAACACAGAAAAAGTAACTGTATGAGAGAGTAAAT	666
Db	724	ATTGACAGTTTTGAAACACAGACAGAACACAGAAAAAGTAACTGTATGAGAGAGTAAAT	783
0Y	667	GTAATTTCTCCACACACTCCAGTTAGAGCTGTATGAACCTATTCACAACTTAATATATG	726
Db	784	GTAATTTCTCCACACACTCCAGTTAGAGCTGTATGAACCTATTCACAACTTAATATATG	843
0Y	727	ATTTTAAATTCAGCAAGTATCAACCTTCAGAAATTCGATTTCCATATTTAAACATGCG	786
Db	844	ATTTTAAATTCAGCAAGTATCAACCTTCAGAAATTCGATTTCCATATTTAAACATGCG	903
0Y	787	ACAGTAAATCCAAAAGAAATATATATGAAAAGAGAGAAAGATATGAGATACACTTTTAA	846
Db	904	ACAGTAAATCCAAAAGAAATATATGAAAAGAGAGAAAGATATGAGATACACTTTTAA	963
0Y	847	GAAATTTTGTAAAGCTGTGGAGACAGGGTGTGTGCAAAATTTGATCACACGATATCAA	906
Db	964	GAAATTTTGTAAAGCTGTGGAGACAGGGTGTGTGCAAAATTTGATCACACGATATCAA	1023
0Y	907	CTTGGAGTTCCGTTGTATACCGAGTAATGAAATCCATGCTTAAATCAGAAAGAAACGA	966
Db	1024	CTTGGAGTTCCGTTGTATACCGAGTAATGAAATCCATGCTTAAATCAGAAAGAAACGA	1083

Oy	967	TTTACCATTTGAAAATTTTATGACAAATCTCTGATATGACAAATTTTCTCATAGCTTTATTC	1026
Db	1084	TTATTCATTCCAAATTTTATGCAAACTTCTGATATGACAAATTTTCTCATAGCTTTATTC	1143
Oy	1027	GCGTGGCGCTCTYGAAGTGTGTATGCGCACATATACGACAGTACATCTCGAATCTTGAT	1086
Db	1144	GCGTGGCGCTCTYGAAGTGTGTATGCGCACATATACGACAGTACATCTCGAATCTTGAT	1203
Oy	1087	TCTGAAACAGATTTGTCTCTTCCCATGATTCGAATGTGCTTAATTTTAAAAGCCTTGAT	1146
Db	1204	TCTGAAACAGATTTGTCTCTTCCCATGATTCGAATGTGCTTAATTTTAAAAGCCTTGAT	1263
Oy	1147	TTTTTAAAGATGATCAGAAATTTTATCAAAAGACAGAAAGCACTTGACAAAGAAATGATA	1266
Db	1264	TTTTTAAAGATGATGAAAGTTTATCAAAAGACAGAAAGCACTTGACAAAGAAATGATA	1323
Oy	1207	AAACATTTTGAACGATGTGAACATGCAATCATATGSAATCCCTTGATGGCTTCAGATTCA	1266
Db	1324	AAACATTTTGAACGATGTGAACATCATATGSAATCCCTTGATGGCTTCAGATTCA	1383
Oy	1287	CGTTTATTTTGATCTTATTTAAACATCAAAAGACCGAGAAGACCACTGATCACCTTGA	1326
Db	1384	CGTTTATTTTGATCTTATTTAAACATCAAAAGACCGAGAAGACCACTGATCACCTTGA	1443
Oy	1327	TCGTCCTTGTCCCTTAATCTCTCCCTCCGCAATATATACACTGACAGATATATATCT	1386
Db	1444	TCGTCCTTGTCCCTTAATCTCTCCCTCCGCAATATATACACTGACAGATATATATCT	1503
Oy	1387	TCCTCGTTAAGATATCCCAAAGAAAAAGTATACACTACGCTGTAAATTCATCTGCAAT	1446
Db	1504	TCCTCGTTAAGATATCCCAAAGAAAAAGTATACACTACGCTGTAAATTCATCTGCAAT	1563
Oy	1447	GGAGACACGACGACACTGACGCTTCGACACCCGAAAGACATGAAATCTACCTCTCT	1506
Db	1564	GGAGACACGACGACACTGACGCTTCGACACCCGAAAGACATGAAATCTACCTCTCT	1623
Oy	1507	TCACCTGTTTTATAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA	1566
Db	1624	TCACCTGTTTTATAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA	1683
Oy	1567	CGCCTCTCTCTGACGACCCAGAAATTAGAACATATCATCTGGACCTCTTTCGACGACAC	1626
Db	1684	CGCCTCTCTCTGACGACCCAGAAATTAGAACATATCATCTGGACCTCTTTCGACGACAC	1743
Oy	1627	CTCGCAAAATGAGTATGAACTCATGAGAGACGACATTTGACCAAAATATGATGATCTCC	1686
Db	1744	CTCGCAAAATGAGTATGAACTCATGAGAGACGACATTTGACCAAAATATGATGATCTCC	1803
Oy	1687	ATGTATGGGATATGTGAAGGTGAAGAAATATAGACCTTAATTCAAAATCATCTGTAAACAGA	1746
Db	1804	ATGTATGGGATATGTGAAGGTGAAGAAATATAGACCTTAATTCAAAATCATCTGTAAACAGA	1861
Oy	1747	TACAGAGATCTTCTCATGCTGTTCAGAGACATTTCAAACGTGTTTGATCAAAAGAAAG	1806
Db	1864	TACAGAGATCTTCTCATGCTGTTCAGAGACATTTCAAACGTGTTTGATCAAAAGAAAG	1923
Oy	1807	GAGTATGATTTATTAATAGTATTTCTATACTGGCTTCATATGACGAGACTGAAACAAAT	1866
Db	1924	GAGTATGATTTATTAATAGTATTTCTATACTGGCTTCATATGACGAGACTGAAACAAAT	1983
Oy	1867	ATTTCGATATGCTTCCACGACGCCCTACCTTGATACCAATACCTGCACATCTCTGCA	1926
Db	1984	ATTTCGATATGCTTCCACGACGCCCTACCTTGATACCAATACCTGCACATCTCTGCA	2043
Oy	1927	AGGCGTTTACAATTTTCTCAATGTTCAACCTTATACGATTTCTGAGAGGAACATCTATTTCA	1986
Db	2044	AGGCGTTTACAATTTTCTCAATGTTCAACCTTATACGATTTCTGAGAGGAACATCTATTTCA	2103
Oy	1987	CCGCTGAAAGATCCATATAAAATTTTCAGAAAGTCTGCGACAGACCAACAAAATGACTCA	2046
Db	2104	CCGCTGAAAGATCCATATAAAATTTTCAGAAAGTCTGCGACAGACCAACAAAATGACTCA	2163

[illegible]

QY 1447 GCAGAGACACAAACCTCAGCCCTCCAGACCAGAACCATTTGAAATCTACTCTCT 1506
DB 1673 GCAGAGACACAAACCTCAGCCCTCCAGACCAGAACCATTTGAAATCTACTCTCT 1614
QY 1507 TCACCTGTTTAAATAAAGTATGCGGTAGCCTATCTCCGGCTAAATACACTTTGTGA 1566
DB 1613 TCACCTGTTTAAATAAAGTATGCGGTAGCCTATCTCCGGCTAAATACACTTTGTGA 1554
QY 1567 CGCCTCTCTGAGCACCAGCAATAGAACATATCATCTGAGACCCCTTTCCAGACACAC 1626
DB 1553 CGCCTCTCTGAGCACCAGCAATAGAACATATCATCTGAGACCCCTTTCCAGACACAC 1494
QY 1627 CTGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1686
DB 1493 CTGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1434
QY 1687 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1746
DB 1433 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1374
QY 1747 TACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1806
DB 1373 TACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1314
QY 1807 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1866
DB 1313 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1254
QY 1867 ATTTTGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1926
DB 1253 ATTTTGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1194
QY 1927 AGCCCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1986
DB 1193 AGCCCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1134
QY 1987 CCCCCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2046
DB 1133 CCCCCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1074
QY 2047 AGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2106
DB 1073 AGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1014
QY 2107 ATAAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2166
DB 1013 ATAAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 954
QY 2167 CTTCTTAACCACTGAAAAAAGTACGCTTTGATATGAGATGATGATGATGATGATGATGATG 2226
DB 953 CTTCTTAACCACTGAAAAAAGTACGCTTTGATATGAGATGATGATGATGATGATGATGATG 894
QY 2227 AGTAAATATCTCCAGAGAGAGTCCAAATTTCCAGAGAAATCGAGAGAAATGATCTTACT 2286
DB 893 AGTAAATATCTCCAGAGAGAGTCCAAATTTCCAGAGAAATCGAGAGAAATGATCTTACT 834
QY 2287 CGAACACAGATGCAAAAGCAGAAAAATGATGATGATGATGATGATGATGATGATGATGATG 2346
DB 833 CGAACACAGATGCAAAAGCAGAAAAATGATGATGATGATGATGATGATGATGATGATGATG 774
QY 2347 AAATGAGAGATCTCAGAGACCTTGTGAGACATGCTACACCTCGAGATTCATGCTCTCA 2406
DB 773 AAATGAGAGATCTCAGAGACCTTGTGAGACATGCTACACCTCGAGATTCATGCTCTCA 714
QY 2407 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2466
DB 713 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 654
QY 2467 CTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2526
DB 653 CTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 594

QY 2527 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2586
DB 593 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534
QY 2587 AGTTGTAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2646
DB 533 AGTTGTAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 474
QY 2647 ATGGCCCTAGAGTGGAGTCCCTGATTAACCAAGCCCTGCTGACTACTTCCCTCTCTTGG 2706
DB 473 ATGGCCCTAGAGTGGAGTCCCTGATTAACCAAGCCCTGCTGACTACTTCCCTCTCTTGG 414
QY 2707 TAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2766
DB 413 TAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 354
QY 2767 AACATGACACCCCTTAGAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2826
DB 353 AACATGACACCCCTTAGAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 294
QY 2827 CCCATTCCACCAAAATTAATCTGAACTCTTCCGAAAAATGGAATTAATGAAATTAGAA 2886
DB 293 CCCATTCCACCAAAATTAATCTGAACTCTTCCGAAAAATGGAATTAATGAAATTAGAA 234
QY 2887 AAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2946
DB 233 AAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 174
QY 2947 GCTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3006
DB 173 GCTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 114
QY 3007 TGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3066
DB 113 TGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 54
QY 3067 TATTTCTTCATCCAACTTAATGTTTAAATGAGATTAATGATAGT 3113
DB 53 TATTTCTTCATCCAACTTAATGTTTAAATGAGATTAATGATAGT 7

RESULT 5
US-08-204-329-2
Sequence 2, Application US/08204329
Patent No. 5710255
GENERAL INFORMATION:
APPLICANT: SHEPARD, H. M.
APPLICANT: MEN, SHU F.
TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
TITLE OF INVENTION: MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,329
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05866
FILING DATE: 14-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: RENE A. FITTS
REGISTRATION NUMBER: 35,136


```

Db 2500 AGCCCTTACAAAGTTCTCTAGTTCCACCCCTACGATTCCTGGAGGGAACATCTATATTTC 2559
Qy 1987 CCCCTGAAGAGTCCATTAATAATTGCAAGAGTCTGCCAAGCAACAAATAATACCCA 2046
Db 2560 CCCCTGAAGAGTCCATTAATAATTGCAAGAGTCTGCCAAGCAACAAATAATACCCA 2619
Qy 2047 AGATCAAGATCTTATGATCAATTTGGTGAATCATTTGGGACCTTGGACAGCTTCAGAAA 2106
Db 2620 AGATCAAGATCTTATGATCAATTTGGTGAATCATTTGGGACCTTGGACAGCTTCAGAAA 2679
Qy 2107 ATAATCAGATGATGATGAACAGCAGCCCTGCTCAAAAAGATGCTGAAGAGCAAC 2166
Db 2680 ATAATCAGATGATGATGAACAGCAGCCCTGCTCAAAAAGATGCTGAAGAGCAAC 2739
Qy 2167 CCTCTAAACCACTGAAAAAATACTACGCTTTGATATTGAAGATCAGATGAGCATGGA 2226
Db 2740 CCTCTAAACCACTGAAAAAATACTACGCTTTGATATTGAAGATGAGCATGAGATGGA 2799
Qy 2227 AGTAAAGATGCTCCAGAGAGTCGCAAAATTTCAGCAGAACTGCGAAGATGACTTACT 2286
Db 2800 AGTAAAGATGCTCCAGAGAGTCGCAAAATTTCAGCAGAACTGCGAAGATGACTTACT 2859
Qy 2287 CGAACAGATGCAAAAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2346
Db 2860 CGAACAGATGCAAAAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2919
Qy 2347 AAATGAGATCTCAGAACCTTGGTGAACATGATGATGATGATGATGATGATGATGATG 2406
Db 2920 AAATGAGATCTCAGAACCTTGGTGAACATGATGATGATGATGATGATGATGATGATG 2979
Qy 2407 CAGATGATGATGAT 2421
Db 2980 CAGATGATGATGAT 2994

RESULT 6
: Sequence 4, Application US/08482627
: Patent No. 5998134
: GENERAL INFORMATION:
: APPLICANT: Lee, Wen-Hua
: TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
: TITLE OF INVENTION: and Regulator
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patientin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,627
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/951,947
: FILING DATE: 28-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-UC 1707
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 4:

```

```

: SEQUENCE CHARACTERISTICS:
: LENGTH: 2994 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 139..2924
: US-08-482-627-4

Query Match 77.6%; Score 2415; DB 2; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ATGTCAAGACTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 66
Db 580 ATGTCAAGACTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 639
Qy 67 ACATGGAACCTTATATATTTGACACAAACCCAGCAGTTCGATATCTGTAATTAATCT 126
Db 640 ACATGGAACCTTATATATTTGACACAAACCCAGCAGTTCGATATCTGTAATTAATCT 699
Qy 127 GCATGGTCTTAAAGATTCTTGTGATCACAATTTTATAGCTAAAGGGAGATTAACAA 186
Db 700 GCATGGTCTTAAAGATTCTTGTGATCACAATTTTATAGCTAAAGGGAGATTAACAA 759
Qy 187 ATGGAAGATGATCTGATGATTTCAATTCAGTTAATGCTATGTCCTTGACTATTTAT 246
Db 760 ATGGAAGATGATCTGATGATTTCAATTCAGTTAATGCTATGTCCTTGACTATTTAT 819
Qy 247 AAATCTCAGCTCCCATGTTCTTCACAAAGAACATATTAACAGCTGTTATACCATAT 306
Db 820 AAATCTCAGCTCCCATGTTCTTCACAAAGAACATATTAACAGCTGTTATACCATAT 879
Qy 307 GGTTCACCTCGAAGACCCAGGCGAGGTGACAGACAGAGATGAGAGATGAGAGAAAGACTA 366
Db 880 GGTTCACCTCGAAGACCCAGGCGAGGTGACAGACAGAGATGAGAGATGAGAGAAAGACTA 939
Qy 367 GAAATGATGACAAAGATTTATGAAATTCCTGTAAAGAACATGATATATATATGAG 426
Db 940 GAAATGATGACAAAGATTTATGAAATTCCTGTAAAGAACATGATATATATATGAG 999
Qy 427 GTGAAAAATGTTTATTTCAAAAAATTTTATACCTTTTATGAAATTCCTGTGACTTGAACA 486
Db 1000 GTGAAAAATGTTTATTTTCAAAAAATTTTATACCTTTTATGAAATTCCTGTGACTTGAACA 1059
Qy 487 TCTAATGACTTCGAGAGTGGAAAAATCTTCTAAACGATACGAAAGAAATTTATCTTAAA 546
Db 1060 TCTAATGACTTCGAGAGTGGAAAAATCTTCTAAACGATACGAAAGAAATTTATCTTAAA 1119
Qy 547 AATAAGATCTAGATGCAAGATTTATTTTGGATCATGATTAATACTCTGAGCTGATCT 606
Db 1120 AATAAGATCTAGATGCAAGATTTATTTTGGATCATGATTAATACTCTGAGCTGATCT 1179
Qy 607 ATAGACAGTTTGAACACAGAGAACACAGAAACGTAAGTGAAGAGTGAAT 666
Db 1180 ATAGACAGTTTGAACACAGAGAACACAGAAACGTAAGTGAAGAGTGAAT 1239
Qy 667 GTATTTCTCCACACACTCCAGTTAGACTGTTATGAACATATCCAACTAATTAATGATG 726
Db 1240 GTATTTCTCCACACACTCCAGTTAGACTGTTATGAACATATCCAACTAATTAATGATG 1299
Qy 727 ATTTAATTCAGCAAGATGATCAACCTTCAGAAATCTGATTTCTATTTTAAACAATGCG 786
Db 1300 ATTTAATTCAGCAAGATGATCAACCTTCAGAAATCTGATTTCTATTTTAAACAATGCG 1359
Qy 787 ACAGTAATCCAAAAGAAAGATATGTAAGAGTGAAGATATAGATATCACTTTTAAA 846
Db 1360 ACAGTAATCCAAAAGAAAGATATGTAAGAGTGAAGATATAGATATCACTTTTAAA 1419
Qy 847 GAAATTTGCTAAAGCTGTGGGACAGAGTGTGTGCAAAATGGATACAGGATACAA 906
Db 1420 GAAATTTGCTAAAGCTGTGGGACAGAGTGTGTGCAAAATGGATACAGGATACAA 1479

```

QY 907 CTTGAGATGCTGTGATTAACGAGTAATGSAATCCATGCTTAATGAGAAAGACGA 966
| | | | |
Db 1480 CTTGAGATGCTGTGATTAACGAGTAATGSAATCCATGCTTAATGAGAAAGACGA 1539
QY 967 TTATCATCAAAATTTTACGAACTCTGAAATGCAACATTTTTCATATGCTTTATG 1026
| | | | |
Db 1540 TTATCATCAAAATTTTACGAACTCTGAAATGCAACATTTTTCATATGCTTTATG 1599
QY 1027 GCGTGGCTGTTGAGTTGTAATGACATATATGACAAAGATGATCGAAGATCTGAT 1086
| | | | |
Db 1600 GCGTGGCTGTTGAGTTGTAATGACATATATGACAAAGATGATCGAAGATCTGAT 1559
QY 1087 TCTGGAACAGATTTGCTTCCATGAGATTCGAATGCTTAATTTAAAGCTTTGAT 1146
| | | | |
Db 1660 TCTGGAACAGATTTGCTTCCATGAGATTCGAATGCTTAATTTAAAGCTTTGAT 1719
QY 1147 TTTTACAAATGATGCAAGTTTATCAAGGAGAAAGCACTTGACAAAGAAATGATA 1206
| | | | |
Db 1720 TTTTACAAATGATGCAAGTTTATCAAGGAGAAAGCACTTGACAAAGAAATGATA 1779
QY 1207 AAACATTTAGACGATGTAACATGCAATCATGCAATCCCTTGACATGCTCTGATTTCA 1266
| | | | |
Db 1780 AAACATTTAGACGATGTAACATGCAATCATGCAATCCCTTGACATGCTCTGATTTCA 1839
QY 1267 CCTTATTTGATCTTATTTAAACATCAAGACCGAAGACCACTGATCACTTTGAA 1326
| | | | |
Db 1840 CCTTATTTGATCTTATTTAAACATCAAGACCGAAGACCACTGATCACTTTGAA 1899
QY 1327 TCTGCTGTGCTCTTATCTCTCTCCAGAAATATCATCTGACGACGAGATATCTT 1386
| | | | |
Db 1900 TCTGCTGTGCTCTTATCTCTCTCCAGAAATATCATCTGACGACGAGATATCTT 1959
QY 1387 TCTGCTGTGATCTCCAAAGAAAGAGTTCACTAGCGCTGTAAATTTCTACTGCAAT 1446
| | | | |
Db 1960 TCTGCTGTGATCTCCAAAGAAAGAGTTCACTAGCGCTGTAAATTTCTACTGCAAT 2019
QY 1447 GCAGAGACAAAGCAACCTGACGCTTCGACGACGAGGCACTTGAAATCTACTGCTT 1506
| | | | |
Db 2020 GCAGAGACAAAGCAACCTGACGCTTCGACGACGAGGCACTTGAAATCTACTGCTT 2079
QY 1507 TCACGTGTTTATTAATAAAAGTATCGGCTATCTCCGCTTAATATCACTTTGTA 1566
| | | | |
Db 2080 TCACGTGTTTATTAATAAAAGTATCGGCTATCTCCGCTTAATATCACTTTGTA 2139
QY 1567 GCGCTGTGCTGAGACCCGAGATTAAGAAATATCATCTGACGCTTTTCACACACAC 1626
| | | | |
Db 2140 GCGCTGTGCTGAGACCCGAGATTAAGAAATATCATCTGACGCTTTTCACACACAC 2199
QY 1627 CTGCAAGATGATGTAATCATGAGACGAGCATTTGACCAAAATTTATGATGTTC 1686
| | | | |
Db 2200 CTGCAAGATGATGTAATCATGAGACGAGCATTTGACCAAAATTTATGATGTTC 2259
QY 1687 ATGTATGCAATGCAAAAGTAAATATGAGCTTAATCAAAATCATTTGTAACGA 1746
| | | | |
Db 2260 ATGTATGCAATGCAAAAGTAAATATGAGCTTAATCAAAATCATTTGTAACGA 2319
QY 1747 TACAAGATCTCTCTATGCTGTTCAGAGACATTCAAACGTTTGTATTAAGAAAG 1806
| | | | |
Db 2320 TACAAGATCTCTCTATGCTGTTCAGAGACATTCAAACGTTTGTATTAAGAAAG 2379
QY 1807 GAGTATGCTTATATATGATCTATTAATGCTGCTTCATGACAGACTGAAACAAAT 1866
| | | | |
Db 2380 GAGTATGCTTATATATGATCTATTAATGCTGCTTCATGACAGACTGAAACAAAT 2439
QY 1867 ATTTTGCAGATGCTTCACACAGCCCTACTCTGACCAATACCTCAATCTCTGCA 1926
| | | | |
Db 2440 ATTTTGCAGATGCTTCACACAGCCCTACTCTGACCAATACCTCAATCTCTGCA 2499
QY 1927 AGCCCTTACAAAGTTTCTAGTTCACCTTACGGAATCTCTGAGGAGACATCTATATTCA 1986
| | | | |
Db 2500 AGCCCTTACAAAGTTTCTAGTTCACCTTACGGAATCTCTGAGGAGACATCTATATTCA 2559

QY 1987 CCCTGAGAGTCCATATATAATTTTCAAGAGGTGCGCAACCAACCAAAATGACTCA 2046
| | | | |
Db 2560 CCCTGAGAGTCCATATATAATTTTCAAGAGGTGCGCAACCAACCAAAATGACTCA 2619
QY 2047 AGATCAAGATCTTAAATCAATTTGATGATCATTTGGGACTTTCGAGAGTTCCAGAAA 2106
| | | | |
Db 2620 AGATCAAGATCTTAAATCAATTTGATGATCATTTGGGACTTTCGAGAGTTCCAGAAA 2679
QY 2107 ATAAATGATGCTATGTAACAGCGGCTGCTGCAAAAGTGAAGTGAAGACGAAC 2166
| | | | |
Db 2680 ATAAATGATGCTATGTAACAGCGGCTGCTGCAAAAGTGAAGTGAAGACGAAC 2739
QY 2167 CTTCTTAAACCACTGAAAAAATGATGATTTGATTAAGGATCAGATGAAGCAGATGGA 2226
| | | | |
Db 2740 CTTCTTAAACCACTGAAAAAATGATGATTTGATTAAGGATCAGATGAAGCAGATGGA 2799
QY 2227 AGTAAACATCTCCAGAGAGTCCAAATTTTCAAGAACTGGCAGAAATGACCTGACT 2286
| | | | |
Db 2800 AGTAAACATCTCCAGAGAGTCCAAATTTTCAAGAACTGGCAGAAATGACCTGACT 2859
QY 2287 CGAACAGATCGAAAAAGCAAAATGATGATGATGATGATGATGATGATGATGATGAT 2346
| | | | |
Db 2860 CGAACAGATCGAAAAAGCAAAATGATGATGATGATGATGATGATGATGATGATGAT 2919
QY 2347 AAATGAGATCTGAGACCTTGTGTGACACTGTGTACACTCTGTGATTCATTTGCTCTCA 2406
| | | | |
Db 2920 AAATGAGATCTGAGACCTTGTGTGACACTGTGTACACTCTGTGATTCATTTGCTCTCA 2979
QY 2407 CAGATGATGATGAT 2421
| | | | |
Db 2980 CAGATGATGATGAT 2994
| | | | |
RESULT 7
US-08-801-092-3
Sequence 3, Application US/08801092
Patent No. 6074850
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
APPLICANT: Wils, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of
NUMBER OF INVENTIONS: Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,092
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Flits, Renee A. 35,136
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

QY	7	ATGCAAGACGTCGTAAAGAAGATGATGATATGTTGGCACTCCTGACGAATTTGGAAG	66
Db	580	ATGCAAGACGTCGTAAAGAAGATGATGATATGTTGGCACTCCTGACGAATTTGGAAG	639
QY	67	ACATGTACACTATATATTTGAGACACACCAGCGAGTTCATFTTCACGAAATTAATCT	126
Db	640	ACATGTACACTATATATTTGAGACACACCAGCGAGTTCATFTTCACGAAATTAATCT	699
QY	127	GCATTGGCTGTAAGATGTCGTGAGACACATTTTATTTAGCTAAAGGGAAGTATACAA	186
Db	700	GCATTGGCTGTAAGATGTCGTGAGACACATTTTATTTAGCTAAAGGGAAGTATACAA	759
QY	187	ATGGAAGATGATCTGCGATATTTGATTCGTAATGCGTATGCTGATCTTTTAT	246
Db	760	ATGGAAGATGATCTGCGATATTTGATTCGTAATGCGTATGCTGATCTTTTAT	819
QY	247	AAATCTCAACGTCGATGTCGCAAGAACCAATTAACAAAGCTGTATATACCAATAT	306
Db	820	AAATCTCAACGTCGATGTCGCAAGAACCAATTAACAAAGCTGTATATACCAATAT	879
QY	307	GCTTCACGTCGAAACCCAGGCGAGGTCGAAAGAGAGTCGACGGATATGCAAAACAC	366
Db	880	GCTTCACGTCGAAACCCAGGCGAGGTCGAAAGAGAGTCGACGGATATGCAAAACAC	939
QY	367	GAAATGATACAAAGAAATTTAGAGTCGTCGTGTAAACATGATATATATATATGAG	426
Db	940	GAAATGATACAAAGAAATTTAGAGTCGTCGTGTAAACATGATATATATATATGAG	999
QY	427	GTCGAAATTCGTTATATTCGAAAAATTTTATACCTTTTGAGATTCCTGTGACGCTG	486
Db	1000	GTCGAAATTCGTTATATTCGAAAAATTTTATACCTTTTGAGATTCCTGTGACCTG	1059
QY	487	TCTTAATGAGATTCGAGAGCTTGAAATTCCTTCTTAACAGATACGAAAGAAATTT	546
Db	1060	TCTTAATGAGATTCGAGAGCTTGAAATTCCTTCTTAACAGATACGAAAGAAATTT	1119
QY	547	AATTAATATCTGATGACGAAGATTTATTTTGGATGATATTAATTAATCTGACAGCT	606
Db	1120	AATTAATATCTGATGACGAAGATTTATTTTGGATGATATTAATTAATCTGACAGCT	1179
QY	607	ATAAGACGTTTGAACACGAGACAAACACGAGAAAAATACCTGTGATGAAAGAG	666
Db	1180	ATAAGACGTTTGAACACGAGACAAACACGAGAAAAATACCTGTGATGAAAGAG	1239
QY	667	GTAATTCCTCCACACCTCCAGCTTATAGAGATCTGTATGACACATTCACAACTTA	726
Db	1240	GTAATTCCTCCACACCTCCAGCTTATAGAGATCTGTATGACACATTCAACTTA	1299
QY	727	ATTTTAAATTCGACAGTGCATCACTTCAGAAAATCTGATTTTCTATTTTAAACA	786
Db	1300	ATTTTAAATTCGACAGTGCATCACTTCAGAAAATCTGATTTTCTATTTTAAACA	1359
QY	787	ACAGTGAATCAAAAGAAAGATATCTGAAAGAGTGAAGGATATAGATACATCTTTAA	846
Db	1360	ACAGTGAATCAAAAGAAAGATATCTGAAAGAGTGAAGGATATAGATACATCTTTAA	1419
QY	847	GAGAAATTTGCTAAAGCTGTGGGACAGGTTGTGTGCAATTTGATCAGCAGATCAAA	906
Db	1420	GAGAAATTTGCTAAAGCTGTGGGACAGGTTGTGTGCAATTTGATCAGCAGATCAAA	1479
QY	907	CTTGAGATTCGCTTGTATTTACCGAGTATATGAAATTCATGCTTAATTCGAGAGA	966
Db	1480	CTTGAGATTCGCTTGTATTTACCGAGTATATGAAATTCATGCTTAATTCGAGAGA	1539
QY	967	TTATCATTCAAAAATTTTAGCAACTTCGTGAATGCAACAATTTTCAATATGTCTTT	1026
Db	1540	TTATCATTCAAAAATTTTAGCAACTTCGTGAATGCAACAATTTTCAATATGTCTTT	1599
QY	1027	GCGTGCGCTTGTAGAGTGTATATGCGCAATATAGCAAGATGATCTCGAGATCTT	1086

Db	1600	GGGTCGCTTTGAGAGTGTGTAAGGCAACATNTAGCAAGAAAGTACATCTCGAATCTTGAT	1659
Oy	1087	TCGTGAACACAAATTTCTCTTCCACATCGATATCGTAAGTACTTAATTTTAAAGCCCTTTGAT	1146
Db	1660	TCGTGAACACATTTCTTCTTCCTCCATGGATATCGTAAGTACTTAATTTTAAAGCCCTTGAT	1719
Oy	1147	TTTTACAAAGTATGTAAGATTTATCCAAACACAGAGGCAATCTGCACAAAGAAATGATA	1206
Db	1720	TTTTACAAAGTATGTAAGATTTATCCAAACACAGAGGCAATCTGCACAAAGAAATGATA	1779
Oy	1207	AAACATTTAGACAGTGTGTAACATCGATTCATGGATACCTTCGATGGCTCTAGATTTCA	1266
Db	1780	AAACATTTAGACAGTGTGTAACATCGATTCATGGATACCTTCGATGGCTCTAGATTTCA	1839
Oy	1267	CCCTTATTTGATGCTTATTTAAACAAATTAAGAGACGGAAGAGCAACATCGATACCCGTGA	1326
Db	1840	CCCTTATTTATCTTATTTAAACATTAAGAGACGGAAGAGCAACATCGATACCCGTGA	1899
Oy	1327	TCGTGGTGTCCCTTAACATCTCCTCCGAGAAATACATCGACGAGATATGATATCTT	1386
Db	1900	TCGTGGTGTCTCTTAACATCTCCTCCGAGAAATACATCGACGAGATATGATATCTT	1959
Oy	1387	TCCTCGTAAAGTCACAAAAGAAAAAGTTCACTACGCGTGTAAATTCCTATCTCAAT	1446
Db	1960	TCCTCGTAAAGTCACAAAAGAAAAAGTTCACTACGCGTGTAAATTCCTATCTCAAT	2019
Oy	1447	GAAGACACAAAGCACTGACGCTTCGACGACGACAGACGATGAAATCTACCTCTCT	1506
Db	2020	GAAGACACAAAGCACTGACGCTTCGACGACGACAGACGATGAAATCTACCTCTCT	2079
Oy	1507	TCACGTTTTATTTAAAAAGTATATGGGTACGATCTCCGGCTAAATACATCTGTGA	1566
Db	2080	TCACGTTTTATTTAAAAAGTATATGGGTACGATCTCCGGCTAAATACATCTGTGA	2139
Oy	1567	GGCGCTCTCTGACAGCAACGAAATTAAGACATATCTCGACGACCTTCCTACAGACAC	1626
Db	2140	GGCGCTCTCTGACAGCAACGAAATTAAGACATATCTCGACGACCTTCCTACAGACAC	2199
Oy	1627	CTGCAAGATACATAGAACATCAAGACAGACAGGATTTGGACAAATTAATGATGCTTCC	1686
Db	2200	CTGCAAGATACATAGAACATCAAGACAGACAGGATTTGGACAAATTAATGATGCTTCC	2259
Oy	1687	ATGTTATGGCATATGCAAAAGTGAAGAAATATACACTTAAATCAAAATCAATTTGAACAGA	1746
Db	2260	ATGTTATGGCATATGCAAAAGTGAAGAAATATACACTTAAATCAAAATCAATTTGAACAGA	2319
Oy	1747	TACAGAGATCTTCTTCATGCTTCACAGAGACATTCAAACGTGTTTGTATCAAAAGAG	1806
Db	2320	TACAGAGATCTTCTTCATGCTTCACAGAGACATTCAAACGTGTTTGTATCAAAAGAG	2379
Oy	1807	GAGTATGATCTTATTTATGATTTCTATAACTCTGGCTCTCTACAGACATGAAAACAAAT	1866
Db	2380	GAGTATGATCTTATTTATGATTTCTATAACTCTGGCTCTCTACAGACATGAAAACAAAT	2439
Oy	1867	ATTTTGGATATGCTCCACAGAGCCGCCCTTACTCTGTACACATTAAGCTCAATCTCTCGA	1926
Db	2440	ATTTTGGATATGCTCCACAGAGCCGCCCTTACTCTGTACACATTAAGCTCAATCTCTCGA	2499
Oy	1927	AGCCCTTACAGTTCTCAGTTCCACCCCTTACGGAATTCCTGTGAGAGCAATCTATATTCA	1986
Db	2500	AGCCCTTACAGTTCTCAGTTCCACCCCTTACGGAATTCCTGTGAGAGCAATCTATATTCA	2559
Oy	1987	CCCGTGAAGATCATTAATAATTTCAAGAGGTCTGCAACACACAAACAAATATGATCTCA	2046
Db	2560	CCCGTGAAGATCATTAATAATTTCAAGAGGTCTGCAACACACAAACAAATATGATCTCA	2619
Oy	2047	AGATCAGAAATCTTATGATCAATTTGGTGAATCATTTGGAGACTTCTGTAGAGTTCCAGAA	2106
Db	2620	AGATCAGAAATCTTATGATCAATTTGGTGAATCATTTGGAGACTTCTGTAGAGTTCCAGAA	2679
Oy	2107	ATTAATCAGATGTATGTACACGCAACCTGTGCTCAAAAGATGCTGTGAAGAGCAAC	2166

Tue Jan 21 10:03:20 2003

us-09-026-459a-36.rni

Page 16

[illegible]

```

i: US-08-959-638-7                                LOCATION: 139..2922

Query Match                                          77.5%: Score 2412: DB 2: Length 2995:
Best Local Similarity 100.0%: Pred. No.: 0:
Matches 2412: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 7 ATCTAAGACTGTGTGAGAACTATGATGTCTTGGTCCATCTGTCCAGAAATTTGGAAG 66
Db 580 ATGTCAAGACTGTGTGAGAAATATGATGTATTTGTTCACATCTTACGAAATTTGGAAG 639
Oy 67 ACATGTGAAGCTTATATATTGTAACAACAACCGACAGCTGGATATACGAAATAATCT 126
Db 640 ACATGTGAAGCTTATATATTGTAACAACAACCGACAGCTGGATATACGAAATAATCT 699
Oy 127 GCATGTGCTTAAAGTTCTTGTGATCATATTTATATACGTAAAGGGAGATATACA 186
Db 700 GCATGTGCTTAAAGTTCTTGTGATCATATTTATATACGTAAAGGGAGATATACA 759
Oy 187 ATGGAAGATAGATGCTATTTGATTTGATTTGATTAAGTATAGTCTCTGTACTATTA 246
Db 760 ATGGAAGATAGATGCTATTTGATTTGATTTGATTAAGTATAGTCTCTGTACTATTA 819
Oy 247 AATGCTACCTCCATCCATGTCTCTCAAGAAAGCAATATATTAACGCTGTTATACCATTA 305
Db 820 AATGCTACCTCCATCCATGTCTCTCAAGAAAGCAATATATATATATATATATATAT 879
Oy 307 GGTTCACCTCGAACAACGAGGAGAGTGCAGAACAGATGTGACGATATGCAAAACCTA 366
Db 880 GGTTCACCTCGAACAACGAGGAGAGTGCAGAACAGATGTGACGATATGCAAAACCTA 939
Oy 367 GAAATGATTCAGAAATTTATGAGATGCTCTGCTGTAAGAACATGATGTATATATATG 426
Db 940 GAAATGATTCAGAAATTTATGAGATGCTCTGCTGTAAGAACATGATGTATATATG 999
Oy 427 GTCAAAATATGTTATATTTCAAAAATTTATATACCTTTATATGATTTCTCTGACAT 486
Db 1000 GTCAAAATATGTTATATTTCAAAAATTTATATACCTTTATATGATTTCTCTGACAT 1059
Oy 487 TCTATATGACTTCCAGAGTTGAAAATCTTTCTTAACGATACGAAGAAATTTCTTAA 546
Db 1060 TCTATATGACTTCCAGAGTTGAAAATCTTTCTTAACGATACGAAGAAATTTCTTAA 1119
Oy 547 AATTAAGATCTAGATGCAAGATTTATTTTGGATCATGATTAACACTCTTCGACTGATCT 606
Db 1120 AATTAAGATCTAGATGCAAGATTTATTTTGGATCATATTAACACTCTTCGACTGATCT 1179
Oy 607 ATATGACAGTTTGGAAACACAGAGAACACACGAAAGAAATGTAACCTTGATGAAGGTAT 666
Db 1180 ATATGACAGTTTGGAAACACAGAGAACACACGAAAGAAATGTAACCTTGATGAAGGTAT 1239
Oy 667 GTATATCTCCACACACTCCAGTTAGAGACTGTTATGAACACTATCAACATTAATGAT 726
Db 1240 GTATATCTCCACACACTCCAGTTAGAGACTGTTATGAACACTATCAACATTAATGAT 1299
Oy 727 ATTTTAAATTOAGCAATGATCAACCTTCGAAATCTGAAATTCCTATTTTAAACAATGC 786
Db 1300 ATTTTAAATTOAGCAATGATCAACCTTCGAAATCTGAAATTCCTATTTTAAACAATGC 1359
Oy 787 ACAGTGAATCAAAAAGAAAGTATATCTGAAAAGAGTGAAGGATATAGATACATCTTAAA 846
Db 1360 ACAGTGAATCAAAAAGAAAGTATATCTGAAAAGAGTGAAGGATATAGATACATCTTAAA 1419
Oy 847 GAGAAATTTCTTAAAGCTGTGGGACAGGTTGTGTGGAATTTGATGCACAGGATACAA 906
Db 1420 GAGAAATTTCTTAAAGCTGTGGGACAGGTTGTGTGGAATTTGATGCACAGGATACAA 1479
Oy 907 CTGTGAGTTCGCTTGTATTAACCGAGTATGGAATTCACATGCTTAAATCAGAAGAAAGCA 966
Db 1480 CTGTGAGTTCGCTTGTATTAACCGAGTATGGAATTCATGCTTAAATCAGAAGAAAGCA 1539
Oy 967 TTATCAATTCAAAATTTTAGCAACTCTGGAATACAACTTTTTCATATATGCTTTATGT 1026

```

Db	1540	TTATCCATTCGAAAAATTTTGGACAAACGTCGAAATGCAACACATTTTTCATATGCTTTATG	1599
Oy	1027	GCCTGCCTCTTAGGCTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAACTCTGAT	1086
Db	1600	GGCGGCCCTCTTAGGCTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAACTCTGAT	1659
Oy	1087	TCCTGACAGATTTGCTTTCCCATGGATTCGAAATGCTCTAAATTTTAAAGCCCTTGAT	1146
Db	1660	TCCTGACAGATTTGCTTTCCCATGGATTCGAAATGCTCTAAATTTTAAAGCCCTTGAT	1719
Oy	1147	TTTTACAAAGTATCGAAAGTTTTATCAGAAGAAAGCACTTATACAAAGAAATGATA	1206
Db	1720	TTTTTACAAAGTATCGAAAGTTTTATCAGAAGAAAGCACTTATACAAAGAAATGATA	1779
Oy	1207	AAACATTTAGAAAGATGTGAAACATCGAAATCAATGGAATCCCTTGATGGCTCGAGATTCA	1266
Db	1780	AAACATTTAGAAAGATGTGAAACATCGAAATCAATGGAATCCCTTGATGGCTCGAGATTCA	1839
Oy	1267	CCTTATTTATGATCTCTATTTAAACAATCAAGAACCCGAAAGACCAACATGACCTTGAA	1326
Db	1840	CCTTATTTATGATCTCTATTTAAACAATCAAGAACCCGAAAGACCAACATGACCTTGAA	1899
Oy	1327	TCCTGCTTGTCTCTTAATCTTCCTCTCCAGAAATATCACTGACGACAGATATGATCTT	1386
Db	1900	TCCTGCTTGTCTCTTAATCTTCCTCTCCAGAAATATCACTGACGACAGATATGATCTT	1959
Oy	1387	TCCTCTTAGATCTCCAAAGAAAGAAAGGTCACTACGCGGTGAATTTCTACTGCAAAAT	1446
Db	1960	TCCTCTTAGATCTCCAAAGAAAGAAAGGTCACTACGCGGTGAATTTCTACTGCAAAAT	2019
Oy	1447	GCAGAGACACAAAGCAACCTCAGCCCTTCAGACCCAGAACGCAATTTGAATCTACCTCTT	1506
Db	2020	GCAGAGACACAAAGCAACCTCAGCCCTTCAGACCCAGAACGCAATTTGAATCTACCTCTT	2079
Oy	1507	TCACGTGTTTATTAAGAAAGTATGCGGTACGCTATCTCCGGCTTAAATACCTTTGTGAA	1566
Db	2080	TCACGTGTTTATTAAGAAAGTATGCGGTACGCTATCTCCGGCTTAAATACCTTTGTGAA	2139
Oy	1567	CGCCTTCTGTCTGAGACCCCAAGATTBAGACATATCATGTGACCCCTTTTCCAGCACCC	1626
Db	2140	CGCCTTCTGTCTGAGACCCCAAGATTBAGACATATCATGTGACCCCTTTTCCAGCACCC	2199
Oy	1627	CTGCAAGATGAGTATGAACTCATGAGAGACAGGCACTTGGACCAATTATGATGCTTCC	1686
Db	2200	CTGCAAGATGAGTATGAACTCATGAGAGACAGGCACTTGGACCAATTATGATGCTTCC	2259
Oy	1687	ATGTATGGCATATGCAAAATGAAAGATATBAGACCTTAAATCAAAATCATTTGTAAACGA	1746
Db	2260	ATGTATGGCATATGCAAAATGAAAGATATBAGACCTTAAATCAAAATCATTTGTAAACGA	2319
Oy	1747	TACAGAGATCTCTCATGCTGTTCAGAGAACCTTCAAAAGTGGTTTGTATCAAAAGAG	1806
Db	2320	TACAGAGATCTCTCATGCTGTTCAGAGAACCTTCAAAAGTGGTTTGTATCAAAAGAG	2379
Oy	1807	GAGTATGATTCATATTATATAGTATTCATTAATCGCTTCATGACAGACTGAAAACAAT	1866
Db	2380	GAGTATGATTCATATTATATAGTATTCATTAATCGCTTCATGACAGACTGAAAACAAT	2439
Oy	1867	ATTTTGCAGTATGCTTCCACACAGGCCCTCAGCTGTACACAAATACCTCACATTCCTGGA	1926
Db	2440	ATTTTGCAGTATGCTTCCACACAGGCCCTCAGCTGTACACAAATACCTCACATTCCTGGA	2499
Oy	1927	AGCCCTTACAAAGTTTCTAGTTACCCCTTACGGAATTCCTGAGAGAACATCTATATTTCA	1986
Db	2500	AGCCCTTACAAAGTTTCTAGTTACCCCTTACGGAATTCCTGAGAGAACATCTATATTTCA	2559
Oy	1987	CCCCGAAAGTCCATATTAATAATTTTCAGAAAGTCTCCCAACACCAACAAATAATGACTCA	2046
Db	2560	CCCCGAAAGTCCATATTAATAATTTTCAGAAAGTCTCCCAACACCAACAAATAATGACTCA	2619
Oy	2047	AGATCAAGAAATCTTAATATCAATTTGGTGAATCAATGGGACCTTGGAAAGTTTCCAGAAA	2106
Db	2620	AGATCAAGAAATCTTAATATCAATTTGGTGAATCAATGGGACCTTGGAAAGTTTCCAGAAA	2679

QY	2107	ATTATCATGATGGATATATATACACGACGACCGGTCTCTAAAGAAAGTGTGGAAGGAAC	2166
Db	2680	ATTAAATCATGATGGATATATATACACGACGACCGGTCTCTAAAGAAAGTGTGGAAGGAAC	2739
QY	2167	CCCTCTAAACCACTGAAAAAACTACGCTTTGATATTTGAAGATTCAGATGAACAGATGGA	2226
Db	2740	CCCTCTAAACCACTGAAAAAACTACGCTTTGATATTTGAAGATTCAGATGAACAGATGGA	2799
QY	2227	AGTAAACATCTCCCGAGGAGGTCCAAATTCTACACAAACTGGCAAAATGACTCTACT	2286
Db	2800	AGTAAACATCTCCCGAGGAGGTCCAAATTCTACACAAACTGGCAAAATGACTCTACT	2858
QY	2287	CGAACACGAATGCAGAAAGCAGAAAAATGAATGATAGCATGGATACCTCAACAAGAGAG	2346
Db	2860	CGAACACGAATGCAGAAAGCAGAAAAATGAATGATAGCATGGATACCTCAACAAGAGAG	2919
QY	2347	AAATGAGAGATTCGAGACCTTGGGAGCACTGTGTACCTCTGGATTCATCTCTCA	2406
Db	2920	AAATGAGAGATTCGAGACCTTGGGAGCACTGTGTACCTCTGGATTCATCTCTCA	2979
QY	2407	CAGATGTGACTG 2418	
Db	2980	CAGATGTGACTG 2991	
RESULT 11			
US-08-328-673A-7			
Sequence 7, Application US/08328673A			
Patent No. 6210939			
GENERAL INFORMATION:			
APPLICANT: Gregory, Richard J.			
Mills, Ken N.			
Maneval, Daniel C.			
TITLE OF INVENTION: Recombinant Adenoviral Vector and			
Methods of Use			
NUMBER OF SEQUENCES: 9			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, Eighth Floor			
CITY: San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94111-3834			
COMPUTER READABLE FORM:			
MEDIUM TYPE: floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/328,673A			
FILING DATE: 25-Oct-1994			
CLASSIFICATION: <Unknown>			
Prior Application DATA:			
APPLICATION NUMBER: US 08/142,669			
FILING DATE: 25-Oct-1993			
APPLICATION NUMBER: US 08/233,669			
FILING DATE: 26-Apr-1994			
ATTORNEY/AGENT INFORMATION:			
NAME: Smith, Timothy S.			
REGISTRATION NUMBER: 35,367			
REFERENCE/DOCKET NUMBER: 016930-000920US			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 576-0200			
TELEFAX: (415) 576-0300			
INFORMATION FOR SEQ ID NO: 7:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 2995 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: CDNA			
FEATURE:			

NAME/KEY: CDS
LOCATION: 139...2925
OTHER INFORMATION: /product="RB"
/note="retinoblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-328-673A-7

Query Match 77.4%; Score 2410.4; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ATGTCAAGACTGTTGAAGAAGTATGATGTTGTCATCTTCAGCAAAATGGAAAG 66
DB 580 ATGTCAAGACTGTTGAAGAAGTATGATGTTGTCATCTTCAGCAAAATGGAAAG 639
QY 67 ACATGTGAACCTATATATTTGACACACACCAGCAGTTCATCTCTACTAAATTTCT 126
DB 640 ACATGTGAACCTATATATTTGACACACACCAGCAGTTCATCTCTACTAAATTTCT 699
QY 127 GCATTTGCTTAAGTTTCTTGATCATTTTATTTAGCTAAAGGGAGATTACAA 186
DB 700 GCATTTGCTTAAGTTTCTTGATCATTTTATTTAGCTAAAGGGAGATTACAA 759
QY 187 ATGAGAGATGATCTGTTGATTTTCATTTCAATGCTATGTCCTTACTATTTAT 246
DB 760 ATGAGAGATGATCTGTTGATTTTCATTTCAATGCTATGTCCTTACTATTTAT 819
QY 247 AAATCTCACCTCCCATGTTGCTCAAGAACCATATTAAGACGCTTTATACCATTA 306
DB 820 AAATCTCACCTCCCATGTTGCTCAAGAACCATATTAAGACGCTTTATACCATTA 879
QY 307 GGTTCACTGACACACACGAGGAGTCAAGACAGAGTGCAGATACCAAAACACTA 366
DB 880 GGTTCACTGACACACACGAGGAGTCAAGACAGAGTGCAGATACCAAAACACTA 939
QY 367 GAAATGATACAGAAATTTATTTGAAGTCTCTGTAAAGACATGATATATATGATG 426
DB 940 GAAATGATACAGAAATTTATTTGAAGTCTCTGTAAAGACATGATATATATGATG 999
QY 427 GTGAAAAATGTTTATTTCAAAATTTTATACCTTTATGAAATCTCTGACACTGTA 486
DB 1000 GTGAAAAATGTTTATTTCAAAATTTTATACCTTTTATGAAATCTCTGACACTGTA 1059
QY 487 TCTAATGACTTCCAGAGTTGAAATCTTCTTAAACGATAGACAGAAATTTATCTTAA 546
DB 1060 TCTAATGACTTCCAGAGTTGAAATCTTCTTAAACGATAGACAGAAATTTATCTTAA 1119
QY 547 AATTAAGATCTAGATGCAAAATTTTGGATCATGATAAACTCTTCAGACTGATCT 606
DB 1120 AATTAAGATCTAGATGCAAAATTTTGGATCATGATAAACTCTTCAGACTGATCT 1179
QY 607 ATAGACAGTTTGAACACAGAGAACACACAGAAAAAGTAACCTGATGAAAGTGAT 666
DB 1180 ATAGACAGTTTGAACACAGAGAACACACAGAAAAAGTAACCTGATGAAAGTGAT 1239
QY 667 GTAATTCCTCACACACTCCAGTTAGAGCTGTTATGACACTTCCAACTAATTAATG 726
DB 1240 GTAATTCCTCACACACTCCAGTTAGAGCTGTTATGACACTAATTAATTAATG 1299
QY 727 ATTTAATTCAGAACTGATCAACCTTCAGAAATCTGATTCCTTTTAACTGTC 786
DB 1300 ATTTAATTCAGAACTGATCAACCTTCAGAAATCTGATTCCTTTTAACTGTC 1359
QY 787 ACAGTGAATCCAAAGAAAGTATCTGAAAAAGATGAAAGATATAGATACATCTTAAA 846
DB 1360 ACAGTGAATCCAAAGAAAGTATCTGAAAAAGATGAAAGATATAGATACATCTTAAA 1419
QY 847 GAGAAATTTGCTAAAGCTGTGTGGACAGGTTGTGTCAAAATGGATACAGCATTA 906
DB 1420 GAGAAATTTGCTAAAGCTGTGTGGACAGGTTGTGTCAAAATGGATACAGCATTA 1479
QY 907 CTGAGATGCTGTATATACGATGATGATCCATGCTTAATCAGAAAGAACGA 966

DB 1480 CTGAGATGCTGTATATACCGAGTAATGAAATCCATGCTTAATCAGAAAGAACGA 1539
QY 967 TTATCCATTCAAATTTTGAACAACTCTGATAGACAAATTTTTCATGCTTTATG 1026
DB 1540 TTATCCATTCAAATTTTGAACAACTCTGATAGACAAATTTTTCATGCTTTATG 1599
QY 1027 GCGTGCCTCTTGAAGTTGTAAATGGCCATATATAGCAGAAATCATCTCGAATCTTGAT 1086
DB 1600 GCGTGCCTCTTGAAGTTGTAAATGGCCATATATAGCAGAAATCATCTCGAATCTTGAT 1659
QY 1087 TCTGACACAGATTTGCTCTTCCCATGAGATCTGAAATGCTTAATTTAAAGCTTTGAT 1146
DB 1660 TCTGACACAGATTTGCTCTTCCCATGAGATCTGAAATGCTTAATTTAAAGCTTTGAT 1719
QY 1147 TTTTACAAAGTATCGAAAGTTTATCAAGACAGAAAGCACTTGACAGAAATGATA 1206
DB 1720 TTTTACAAAGTATCGAAAGTTTATCAAGACAGAAAGCACTTGACAGAAATGATA 1779
QY 1207 AAACATTTAGACGATGGAACATGCAATCATGGAATCCCTGATGCTCTCAGATTCA 1266
DB 1780 AAACATTTAGACGATGGAACATGCAATCATGGAATCCCTGATGCTCTCAGATTCA 1839
QY 1267 CCTTATTTGATCTTATTAACATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1326
DB 1840 CCTTATTTGATCTTATTAACATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1899
QY 1327 TCTGCTTCTCTTAATCTCTCTCCAGAAATATCAACATGACAGAGATATGATCTT 1386
DB 1900 TCTGCTTCTCTTAATCTCTCTCCAGAAATATCAACATGACAGAGATATGATCTT 1959
QY 1387 TCTCTGTAGATCTCCAAAGAAAAAGTTCACTACGCTGTAAATCTCTACGCAAT 1446
DB 1960 TCTCTGTAGATCTCCAAAGAAAAAGTTCACTACGCTGTAAATCTCTACGCAAT 2019
QY 1447 GCAGAGACAAAGCAACCTCCAGACCTTCCAGACCAAGAGAGAGAGAGAGAGAGAGAG 1506
DB 2020 GCAGAGACAAAGCAACCTCCAGACCTTCCAGACCAAGAGAGAGAGAGAGAGAGAG 2079
QY 1507 TCACGTGTTTATTAATAAAGTATATGCGGTAGCTATCTCGGCTTAATCACTTTTGAA 1566
DB 2080 TCACGTGTTTATTAATAAAGTATATGCGGTAGCTATCTCGGCTTAATCACTTTTGAA 2139
QY 1567 GCGCTTGTCTGACACCCAGAAATTAGACATATCATCTGACCCCTTTCACACACAC 1626
DB 2140 GCGCTTGTCTGACACCCAGAAATTAGACATATCATCTGACCCCTTTCACACACAC 2199
QY 1627 CTGCAAGATGATGAATGAATCATGAGACAGGCAATTTGACCAAAATATGATGTCTC 1686
DB 2200 CTGCAAGATGATGAATGAATCATGAGACAGGCAATTTGACCAAAATATGATGTCTC 2259
QY 1687 ATGTATGCAATTCGCAAGAGTGAAGATATAGACCTTTAAATTCAAATATATTTAG 1746
DB 2260 ATGTATGCAATTCGCAAGAGTGAAGATATAGACCTTTAAATTCAAATATATTTAG 2319
QY 1747 TACAAAGATCTTCCATATGATCTCTGAGAGACATTCAAACGTTTATCAAGAAAG 1806
DB 2320 TACAAAGATCTTCCATATGATCTCTGAGAGACATTCAAACGTTTATCAAGAAAG 2379
QY 1807 GAGTATGATCTTATATATATATATTAATCTCGCTTCTCATATGACAGACTGAAAAAT 1866
DB 2380 GAGTATGATCTTATATATATATATTAATCTCGCTTCTCATATGACAGACTGAAAAAT 2439
QY 1867 ATTTTCAGATGCTCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1926
DB 2440 ATTTTCAGATGCTCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2499
QY 1927 AGCCCTTAAGATTCCTGATTCACCTTACGATTCCTGAGAGAGAGATCATATTTTCA 1986
DB 2500 AGCCCTTAAGATTCCTGATTCACCTTACGATTCCTGAGAGAGAGATCATATTTTCA 2559
QY 1987 CCCCTGAAGATTCATATATAATTTTCAGAGGCTTGCACCAACCAAAATATGATCTCA 2046
DB 2560 CCCCTGAAGATTCATATATAATTTTCAGAGGCTTGCACCAACCAAAATATGATCTCA 2619

QY	2047	AGATCAAGAAATTGTAAGTCAATGAGGATCATTCGGGACTTGTGGAAAGTCCAGAA	2106
Db	2620	AGATCAAGAACTTAACTAGTTCATATGGTGAATCATTCGGGACTTGTGGAAAGTCCAGAA	2679
QY	2107	ATTAATCAGATGGTATGTAAACAGCAGCGTGTCTCAAAAGAAAGTGTCTGAGGAGCAAC	2166
Db	2680	ATTAATCAAGATGGTATGTAAACAGCAGCGTGTCTCAAAAGAAAGTGTCTGAGGAGCAAC	2739
QY	2167	CTCTCTAAACCACTGAAAAAACTACACCTTGTGATTTGAAGGATCAGATGACAGATGGA	2266
Db	2740	CTCTCTAAACCACTGAAAAAACTACACCTTGTGATTTGAAGGATCAGATGAGATGGA	2739
QY	2227	AGTAAACATCTCCCGAGGAGATGCCAATTTGACGGAATCTGGAGAAATGACTTCTACT	2286
Db	2800	AGTAAACATCTCTCCCGAGGAGATGCCAATTTGACGAGAAATCTGGAGAAATGACTTCTACT	2859
QY	2287	CGAACCGAATGCAAAAGCAGAAAAATGAATGATAGCATGGATACCTTAAACAAGAGAGG	2346
Db	2860	CGAACCGAATGCAAAAGCAGAAAAATGAATGATAGCATGGATACCTTAAACAAGAGAGG	2919
	2347	AAATGAGATCTCAGAGACCTTGGTGACACTGTGACACCTCTGGATTCTATCTCTCA	2406
Db	2920	AAATGAGATCTCAGAGACCTTGGTGACACTGTGACACCTCTGGATTCTATCTCTCTCA	2979
QY	2407	CAGATGTGACTG 2418	
Db	2980	CAGATGTGACTG 2991	

RESULT 12
 US-07-708-962-1
 Sequence 1, Application US/07708962
 Patent No. 5262321
 GENERAL INFORMATION:
 APPLICANT: Livingston, David M.
 APPLICANT: Even, Mark E.
 TITLE OF INVENTION: Tumor Suppressor
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Choate, Hall & Stewart
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/708, 962
 FILING DATE: 19910531
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kennedy, Bill
 REGISTRATION NUMBER: 33,407
 REFERENCE/DOCKET NUMBER: DFCI 209
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-5020
 TELEFAX: (617) 227-7566
 TELEX: 289374
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2808 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-07-708-962-1

Query Match	2.2%;	Score 68.8;	DB 1;	Length 2808;
Best Local Similarity	53.1%;	Pred. No. 3.6e-07;		
Matches 170;	Conservative	0;	Mismatches 147;	Indels 3;
				Gaps 1;

Qy	1481	AGAGGCGATGAAATACACACGCTCTTCCACTGTTTATATAAAAAGGTACGGCTAGCCT	1540
Db	1340	ACAGGCGAAGAGAACTGGGCGCTGTAGCACTATTATTACAGAAAGGTATATCATTTGGCA	1999
Qy	1541	ATCTCCGCTAAATATCACTTTTGGAAAGCGCTCTGTGAGACACCCGAAATATGAACATA	1600
Db	2000	GCTGTACGCTTACGTATCAATCACTG---CTAAACTGGATGTTTCAATAGATTCACAGGA	2056
Qy	1601	TCACTGAGCCCTTTCTCAGACACCCCTGCAGATGATGACATCAAGAGACAGC	1660
Db	2057	AGATATGACACGCTTTTGCATATTCACCTTATGCTACCTGCTGATCTATATTAAGACAGCG	2116
Qy	1661	AATTTGACCAATTTATGATGTGTTCCATGTATGACATATGCAAGTCAGAGATATATGACC	1720
Db	2117	ATTGTGATGAGCTCTCTCTTGTGCTCTTTATATATGACCAAGTATACAAAGAGAGAA	2176
Qy	1721	TTTAATTTCAAATATCATTTATACACGATACAGAGATCTCTCATGCTGTTTCAGAGACAT	1780
Db	2177	GAACTTTTACAGAAATTTATGAAAGATTATAGGAATACACCCCAAGCTATATATGTCAGAT	2236
Qy	1781	TCAACGCTGTTTGATCAA	1800
Db	2237	ATGAGAGTGTCTGCTGAAA	2256

RESULT 13
 US-08-106-493A-1
 Sequence 1, Application US/08106493A
 Patent No. 5457049
 GENERAL INFORMATION:
 APPLICANT: Antonio Giordano
 TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRB2,
 TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODINGS
 TITLE OF INVENTION: THEREFOR"
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Temple University Of The Commonwealth
 STREET: 406 University Services Building
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/106,493A
 FILING DATE: August 12, 1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mullins, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 6056-188
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 TELEX: No. 5457049e
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3249 base pairs
 type: nucleic acid
 STRANDEDNESS: Single

Tue Jan 21 10:03:20 2003

us-09-026-459a-36.rn1

Page 21

```

; NAME/KEY: CDS
; LOCATION: 70..3489
US-08-832-883-1

```

Query Match	2.2%;	Score 68.2;	DB 1;	Length 4853;
Best Local Similarity	53.0%;	Pred. No. 6e-07;		
Matches 170;	Conservative 0;	Mismatches 148;	Indels 3;	Gaps 1;

QY	1481	AGGACCATGAATCTACCTCTCTTCACGTGTTTATATAAAATGATGCGGACGT	1540
Db	2552	ATATACCCAGAGAGACAGCTCTTTTCCGCTTTCTTTGAAAGGTATACATTTTAGAG	2611
QY	1541	ATCTCGGCGTAAATACACTTTTGTGAACGCCCTTCTGTCTGAGCACCCAGAAATTAGAACATA	1600
Db	2612	CTGTCGCCCTTCGGGATCTGTGTG ---CCAAACTGAGATATTTTCAGATATATTTAGAGAAA	2668
QY	1601	TCATCTGAGACCTTTTTCACACACACCCTCAGATAGTAGTATGACATGATGAGACAGC	1660
Db	2669	AAATCTGACCTGGTTTGAAATCTTCATTAATTCAGTGTCTGAACCTATATGATGAGCAGAC	2728
QY	1661	ATTGTGACCAATTTATGATGTGTTCATGTATNGCATATGCAAAATGAAAGATATAGACC	1720
Db	2729	ATCTGAGACCATTTATATATGTGTGCCATTTATGTATGTCGAAAGGTCCACAAAAGAAGTAA	2788
QY	1721	TTAATTTCAAAATCATGTATACAGCATATACAGAGATCTTTCATGCTGTTCAGAGACAT	1780
Db	2789	AGTCCTTCCAGAACATATATCATCGTTGTTATTAGACTCAGCCGACGAGCCGAGACCGAGTGT	2848
QY	1781	TCAAACGCTTTTGATATCAAG	1801
Db	2849	ATAGAGAGTGTTTGATATAAG	2869

```
Search completed: January 17, 2003, 18:22:00
Job time : 106.88 secs
```

10

11

12

13

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:58 | Search time 250.854 Seconds

(without alignments) 7011.280 Million cell updates/sec

Title: US-09-026-459a-37

Sequence: 1 MSRLKKYDVLPAFLSKLER.....TRMKOKMNDSDTSNKEEK 781

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

ched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL-frame+ p2n.model -DEV-xlh
-O/-cgr2.1/USPTO.spool/US09026459/runat.16012003.152137.23299/app.query.fasta.1.13467
-DB-N Geneseq 101002 -OPMT-fastestp -SUPER-orig -MINMATCH-0.1 -LOCPCT=0
-LOOPEXT=0 -UNITS-bits -START=1 EMD=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -TRX-SCORE-pct -TRX-MAX=100 -TRX-MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pic -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR-US09026459.ecgn.1.1.2527-efunat.16012003.152137.23299 -NCPV=6 -ICPV=3
-NO_XLPHY -NO_MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4017	100.0	2994	11 AA004713	Cancer suppressing
2	4017	100.0	2994	14 AA041545	Retinoblastoma gen
3	4017	100.0	2994	19 AAV40004	Retinoblastoma pro
4	4017	100.0	2994	21 AAT40287	Wild type human re
5	4017	100.0	2995	20 AAX90350	Human p110-RB reti
6	4017	100.0	2995	20 AAX00737	cDNA encoding a re
7	4017	100.0	2995	22 AAH25755	Retinoblastoma tum
8	4017	100.0	2995	22 AAD04474	Retinoblastoma tum
9	4017	100.0	2995	23 ABL50904	Retinoblastoma tum
10	4017	100.0	3113	19 AAV58445	Modified retinobla
11	4017	100.0	3218	19 AAV54991	DNA sequence of th
12	4017	100.0	3233	15 AA072690	Retinoblastoma 94k
13	4017	100.0	3266	19 AAV58444	Modified retinobla
14	4017	100.0	3323	19 AAV58445	Modified retinobla
15	4017	100.0	3323	19 AAV58446	Modified retinobla
16	4017	100.0	3392	19 AAV58446	Modified retinobla
17	4017	100.0	3455	19 AAV58441	Modified retinobla
18	4017	100.0	3461	19 AAV58447	Modified retinobla
19	4017	100.0	3554	19 AAV58452	Modified retinobla
20	4017	100.0	3555	19 AAV58440	Modified retinobla
21	4017	100.0	3555	19 AAV54990	DNA sequence of th
22	4017	100.0	4839	21 AAT29391	Human retinoblasto
23	4017	100.0	4839	21 AAT28644	Human androgen rec
24	4017	100.0	4839	24 ABL62873	Breast cancer rela
25	4014	99.9	4597	9 AAN81369	Human retinoblasto
26	4013	99.9	2995	16 AAO90059	Retinoblastoma tum
27	4013	99.9	4597	15 AA070536	Human retinoblasto
28	4011	99.9	4740	24 ABR66079	Human retinoblasto
29	4010	99.8	4597	20 AAX04501	Human retinoblasto
30	4002	99.6	2995	16 AAO86398	Human Rb10 cDNA.
31	3903	97.2	5056	10 AAN90489	CDNA of human reti
32	3875	96.3	4579	9 AAN81261	Probe for retinobla
33	3850	95.8	3347	19 AAV58446	Modified retinobla
34	3674.5	91.5	3377	19 AAV58451	Modified retinobla
35	3667.5	91.3	3383	19 AAV58450	Modified retinobla
36	3550	88.4	3161	19 AAV58449	Modified retinobla
37	1761.5	43.9	18303	20 AAX04502	Human retinoblasto
38	1685.5	42.0	18177	10 AAN90490	DNA of human retin
39	772	19.2	3960	24 ABR68440	Human DNA sequence
40	771	19.2	4130	24 AAS94981	Human DNA sequence
41	756	18.8	2808	13 AAO32665	Nearly complete pi
42	729.5	18.2	4853	24 ABR64660	Human cDNA diffe
43	728.5	18.1	3249	16 AAO82748	PRD2 retinoblastom
44	605.5	15.1	3291	23 AAS83193	DNA encoding novel
45	519.5	12.9	3210	23 ABL12861	Drosophila melanog

ALIGNMENTS

RESULT 1

AA004713 standard; cDNA; 2994 BP.

AA004713:

11-OCR-1990 (first entry)

Cancer suppressing gene (CSG).

Cancer: cancer suppressing gene; CSG; 13q14; retinoblastoma;

RB; ds.

Homo sapiens.

Key Location/Qualifiers
139..2922 /tag a

XX MO9005180-A.
XX 17-MAY-1990.
XX 30-OCT-1989; 89WC-0004808.
XX 31-OCT-1988; 88US-0265829.
XX (REGC) UNIV OF CALIFORNIA.
XX Lee WH, Huang HS;
XX WPI: 1990-178822/23.
XX P-PSDB: AAR05305.
XX
XX Controlling cancer -
XX by replacing ineffective cancer suppressing gene with cloned,
XX active gene.
XX
XX Claim 35; Page 86; 105pp; English.
XX Gene is taken from human chromosome 13q14 retinoblastoma (RB) CDNA.
XX By installing a working CSG, safe and specific treatment and
XX prophylaxis can be given to cancer patients.
XX
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other:

Alignment Scores:
Pred. No.: 0 Length: 2994
Score: 4017.00 Matches: 781
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-026-459a-37 (1-781) x AAR004713 (1-2994)
OY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
DB 580 ATGTCAGAGACTGTGAAGAGATGATGATGTTGGACTCTTCAGCAAAATGGAAAG 639
OY 21 ThrCysGluLeuLeuTyrLeuThrGlnProSerSerSerLysThrGluLysAsnSer 40
DB 640 ACATGTGAATTAATTAATTTGACCAACACCGAGTTCATATCTACGAAATTAATTC 699
OY 41 AlaLeuValLeuLysValSerTrpLysPheLeuLeuAlaLysGlyGluValLeuGln 60
DB 700 GCATTGGGTCTAAAGTTCTCTGATCCATTTTATAGCTAAAGGGAGATATTACAA 759
OY 61 MetGluAspAspLeuValLysSerPheGlnLeuMetLeuCysValLeuAspTyrPheLe 80
DB 760 ATGGAAGATGATCTGTGATTCATTTCATGATATCTATGTCTCTGACATATTAT 819
OY 81 LysLeuSerProPheMetLeuLysGluProTyrLysThrAlaValLeuProLysAsn 100
DB 820 AAACCTCTACCTCCCATGTTGCTCAAGAACCTATTAAGAGCTGTATACCCATTAT 879
OY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
DB 880 GGTTACCTCTCAACACCGCAGCGACGACGAACAGAGTGCACGATACCAAAACAATA 939
OY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
DB 940 GAAATATGATACAAAGATATGAAAGTCTCTGTAAGAAACATGATATATATAGATAG 999
OY 141 ValLysAsnValTyrPheLysAsnPheLeuProPheMetLysSerLeuGlyLeuValThr 160
DB 1000 GTGAAAAATGTTTATTTCAAAATTTTATACCTTTATGATATCTCTGATTTTACA 1059
OY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluLysLeuLys 180
DB 1060 TCTATATGACTTCCAGAGGTTGAAATCTTTCTAAACGATAGAGAAATTTATCTTAAA 1119

OY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
DB 1120 AATAAAGATCTAGATGCAAGATTTTGTGATCATGATTAAGCTCTCAGACTATTC 1179
OY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
DB 1180 ATAGACAGTCTTTGAACACAGACAGAACACGAAAGATACCTTGATGAAAGAGTGAT 1239
OY 221 ValIleProPheHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMet 240
DB 1240 GTAACTCTCCACACACTCCAGTAGACCTGTATGACACATATCCAAATATATGATG 1299
OY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuLysThrPheAsnAsnCys 260
DB 1300 ATTTTAATTCAGCAGAGTATCAACCTTCAGAAATCTGATTTCCATTTTAAACATGC 1359
OY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 1360 ACAGTGAATCCAAAAGAAAGATATCTGAAAGAGTGAAGATATAGATACATCTTTAAA 1419
OY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
DB 1420 GAGAAATTTGCTAAAGCTGGGACAGGTTGTGTGAAATTCGATCCACGCGATACAA 1479
OY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
DB 1480 CTTGGAGTTCCTGTATTTACCGAGTAAATGGAATCCATGCTTAATACGAAGAAACGA 1539
OY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
DB 1540 TTTATCATTTCAAAATTTTATAGCAACCTTCTGAATGACAACTTTTCAATATGCTTAT 1599
OY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
DB 1600 GCGTCGCTCTTGAGGTGTATATGCGCACATATAGCAAGATCATCTCAGAAATCTGAT 1659
OY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
DB 1660 TCTGAGACAGATTTGCTCTCCATGATCTGAAATGCTTAATTTAAACCTTTAT 1719
OY 381 PheTyrLysValIleGluSerPheIleLysAlaGluIleAsnLeuThrArgGluMetIle 400
DB 1720 TTTTCAAAAGTATGCAAGTTTATATCAAGACAGAAAGCCAACTTGACAGAAATGATA 1779
OY 401 LysHisLeuGlnArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
DB 1780 AAACATTTTGAACGATGGAACATCATGAAATCCCTTCATGCTCTCAGATTTCA 1839
OY 421 ProLeuPheAspLeuLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
DB 1840 CTTTATTTGATCTTATTAACATCAAGACGAGAAAGACCAACATGATCACTTCA 1899
OY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetLysLeu 460
DB 1900 TCTGCTTCTCTTAACTTAACTTCTCTCAGATTAACATCACTGACAGATATATGATCT 1959
OY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
DB 1960 TCTCTGTAAGATCTCCAAAGAAAGTTCAACATACGCGGTATTAATCTACCTCAAT 2019
OY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerSerLeu 500
DB 2020 GCAGAGACAAAGCAACCTCAGCTTCCACAGACAGACATGAAATCTACCTCTCT 2079
OY 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
DB 2080 TCACGTGTTTAAATAAAGTGTATCGGCTAGCCATCTCCGGCTAATAATCACTTTGTGA 2139
OY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
DB 2140 GCGCTTGTGTGACACCCAGAAATATGAAATATATCTGACCCCTTTTCCAGCACACC 2199

Db 940 GAAATGATACAGAAATTAATGAGTTCCTGTAAGAACATGAAATGTAATATAGATGAG 999
Qy 141 VALLYSASNVALTYRPhelysasnPhelIleProPhemeTasnSerleuGluValThr 160
Db 1000 GTGAAAAATGTTATTTCAAAAAATTTTAACTTTTATATATCTCTTGAGACTGTGAACA 1059
Qy 161 SerAsnGluValProGluValGluAsnLeuSerArgTyrGluGluIleTyrLeuLys 180
Db 1060 TCTAATGAGACTCCAGAGGTGAAAAATCTTTCTTAAACGATACAGAAATTTATCTTAA 1119
Qy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
Db 1120 AATAAAGATCTAGATCAAGATTAATTTTGGATCATGATATAAACTCTTGACACTGATTTCT 1179
Qy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
Db 1180 ATGAGACGTTTGAACACAGAGAACCCAGAAAAAGTAACCTTGATGAAAGGTGGAAT 1239
Qy 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
Db 1240 GTAAATTCCTCCACACACTCCAGTTAGAGACTGTATGACACTATCCAAACAATTAATGATG 1299
Qy 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnGly 260
Db 1300 ATTTTAATTCAGCAAGTGTATCAACCTTCAGAAAAATCTGATTTCTTAATTTAACTGTCG 1359
Qy 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
Db 1360 ACAGTGAATCCAAAGAAATATCTGATAAAGAGTAAAGATATAGATATCATCTTTAA 1419
Qy 281 GluLysPheAlaLysAlaValGluGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
Db 1420 GAGAAATTTGCTAAGCTGTGGGACAGGTTGTGCGAAATTTGATGATCAGCATCAAA 1479
Qy 301 LeuGluValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluValArg 320
Db 1480 CTGGAGACTGCTGTGTATACCGAGTAATGAAATCCATGCTTAAATCAGAAAGAAAGCA 1539
Qy 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
Db 1340 TTATCCATTCAAAATTTTACCAAACTTCTGATGACAACTTTTTCATGCTCTTATATG 1599
Qy 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
Db 1600 GCGGCGCCTGTGAGTTGTAATGCGCACATATGACAGAAATCATCTCGAAATCTTGAT 1659
Qy 361 SerLysThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
Db 1660 TCTGGAACAGATTTGTCTTCCCATGGAATTCGTGAATGTCTTAATTTAAAAACCTTGAT 1719
Qy 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluAsnLeuThrArgGluMetIle 400
Db 1720 TTTTACAAGGATCGAAAGTTTATCAAAAGCAGAAAGCAAACTTGACAAAGAAATGATA 1779
Qy 401 LysHisLeuGluArgCysGluHisArgIleMetClnSerLeuAlaThrPheSerAspSer 420
Db 1780 AAACATTTAGACGATGTGAACATCGAATCATGGAATCCCTTGATGCTCTCGATGATCA 1839
Qy 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGluProThrAspHisLeuGlu 440
Db 1840 CCTTTATTTGATCTTATTTAAACATCAAAAGCAGCAGAGAACCACTGATCACTTGAA 1899
Qy 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db 1900 TCTGCTGTCTCTTAATCTCTCTCCAGAAATATCATCACTGACAGAGATATGATCTT 1959
Qy 461 SerProValArgSerProLysLysGlySerThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCCTGTAAATCTCCAAAGAAAAAGTTCACTAGCGGTGTAATTTCTACTGCAAAAT 2019
Qy 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGAGACACAAGCACTGACCTTCACAGACCAAGAAAGCAATGGAATGATGATCTCTT 2079

Qy 501 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
Db 2080 TCACGTTTATTAATAAAAGTATATCGGTATGCTATCTCCGGCTAAATATACCTTTGTGAA 2139
Qy 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGlnHisThr 540
Db 2140 CGCCTTCTGTCTGAGCACCCAGAAATTAGAACATATCATCTTGAGACCTTTTCCAGCACCC 2199
Qy 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
Db 2200 CTGCAGAAATGATGAACTCATGAGACAGACAGCAATTTGGACCAAAATATGATGTCTTCC 2259
Qy 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db 2260 ATGATGGAATGCAAAAGTGAAATGAAATATGACCTTAATTCAAAATCATGATTAACAGCA 2319
Qy 581 TyrLysAspLeuProHisAlaValGluGlnThrPheLysArgValIleLysGluGlu 600
Db 2320 TTCAAGGATCTTCCATCGCTGTTCAGAGACATTTCAACCGTGTTCATCAAAAGAAAGAG 2379
Qy 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db 2380 GAGTATGATTTCTATTTATGATTTCTATTAACTCGGCTTTCATGACAGAGACTGAAACAAT 2439
Qy 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTGAGATATGCTTCCACAGCGCCCTGACTGTGACCAAAATCCTCACATTCCTCGA 2499
Qy 641 SerProTyrLysPheProSerSerProLeuArgIleProGluGluAsnIleTyrIleSer 660
Db 2500 ACCCTTCAAACTTCTGATTCACCTTACCGATCTCTGAGGGAACATCTTATATTTCA 2559
Qy 661 ProLeuLysSerProTyrLysIleSerGluGluLeuProThrProThrLysMetThrPro 680
Db 2560 CCCCTGAAGATGCCATATAAAATTTACAGAGGTCTGCCAACCCAAAGAAATGACTCCA 2619
Qy 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
Db 2620 AGATCAAGAAATCTGTATGATCAATGTGTAAATCATTCGGGAACTTCGAGAAATTCAGAAA 2679
Qy 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluIleSerAsn 720
Db 2680 ATTAATCAGATGTATGTATGACAGCCACCTGTGCTCAAAAGAAAGTCTGAAGAAAGCAAC 2739
Qy 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740
Db 2740 CTTCTTAACCACTGAAAAAACTACGCTTGTATTTGAAGCATCAGATGAAGACGATGGA 2799
Qy 741 SerLysHisLeuProGluLysSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
Db 2800 AGTAAACATCTCCAGAGATCCAAATTTCAAGCAAAATGCGCAAAATGACTTCTACT 2859
Qy 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
Db 2860 CGAGACGGAATCGAAAGAGAAAGAAATGATATGATATGATATGATATGATATGATATG 2919
Qy 781 Lys 781
Db 2920 AAA 2922
RESULT 3
AAV40004
ID AAV40004 standard; DNA; 2994 BP.
XX
AC AAV40004;
XX
DT 15-FEB-1999 (first entry)
XX Retinoblastoma protein RB.
DE
XX Retinoblastoma protein RB.
KW Retinoblastoma protein RB; E2F; transcription factor; human; bladder cancer; restenosis; angioplasty; diabetic retinopathy;

KM thyroid hyperplasia; Grave's disease; psoriasis;
 KM benign prostatic hyperplasia; Li-Fraumeni syndrome;
 KM peripheral vascular disease; therapy; ss.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 139..2925
 FT /+tag- a
 XX
 XX W09821228-A1.
 XX
 XX 22-MAR-1998.
 XX
 XX 13-NOV-1997; 97MO-US21821.
 XX
 XX 14-FEB-1997; 97US-0801092.
 PR 15-NOV-1996; 96US-0751517.
 XX
 PA (CANU-) CANU1 INC.

Antelman D, Gregory RJ, Willis KN;

DR WPI; 1998-297858/26.

DR P-PSDB; AAM62465.

XX
 XX
 PT New fusion polypeptide of, e.g. transcription factor - used to
 PT treat, e.g. hyper-proliferative disease such as cancer and
 PT retinoblastoma

Example 1; Fig 2A; 91pp; English.

XX This nucleotide sequence includes a coding region for retinoblastoma
 CC protein Rb (see AAM62465). A new claimed polypeptide is a fusion of:
 CC (1) a transcription factor (TF) comprising a DNA binding domain,
 CC and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
 CC suppression domain. Also new are: (1) a nucleic acid encoding the
 CC fusion protein, and (2) expression vectors containing such DNA.
 CC The fusion protein, particularly expressed from gene therapy
 CC vectors (especially adenovirus vectors), is used to treat
 CC hyperproliferative conditions, specifically cancer (particularly of
 CC the bladder) or restenosis (after angioplasty), but also diabetic
 CC retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
 CC benign prostatic hyperplasia, Li-Fraumeni syndrome and peripheral
 CC vascular disease. Tissue-specific expression of RbF-Rb fusions is
 CC provided. The fusion proteins are more effective in repressing
 CC transcription of the E2F promoter than Rb alone and cause cell cycle
 CC arrest in a variety of cells.

Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 2994
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0

US-09-026-459A-37 (1-781) x AAV40004 (1-2994)

QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
 DB 580 ATGTAAACACTGTTGAAAGAGATGATGATTTTTCACCTCTTACGCAAAATGGAAAGG 639
 QY 21 ThrCysGluLeuLeuLysLysTyrGlnProSerSerSerLysSerThrGluLeuAsnSer 40
 DB 640 ACATGCTGAACCTTATATATTTGACCAACCCAGAGTTCCATATCACTCAAAATTAATTTCT 699
 QY 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGluValLeuGlu 60
 DB 700 GCATTGGTGCTAAAGATTCTTGATCACAATTTTATTTAGCTAAAGGGGAAGTATTACAA 759

QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
 DB 760 ATGGAAGATGATCGTGGATTTCAATTCATGATTAAGCTATGCTGCTGATATTATT 819
 QY 81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
 DB 820 AAACCTCACCTCCCATGTTGCTCAAAAGAACCATATAAAGAGCTGTATACCATTAAT 879
 QY 101 GlySerProArgTrpProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGluLeu 120
 DB 880 GGTTCACCTCGAACACCCAGGCGAGACAGAGGAGGCGAGATGCAAAACCACTA 939
 QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
 DB 940 GAAATGATACCAAGAAATTAATGAAGTTCTCTGAAAGAACATGATTAATATGATGAG 999
 QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr 160
 DB 1000 GTGAAAATGTTTATTTCAAAATTTTATACCTTTATGATTCCTTGACCTGTTGAC 1059
 QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluIleTyrLeuLys 180
 DB 1060 TCTAATGACCTCCAGAGGTTGAAAAATCTTCTAAACGATACGAAGAAATTTATCTTAA 1119
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 DB 1120 AATTAAGATCTAGATGCAAGATTTATTTTGATCATGATTAACCTTCACACATGATCT 1179
 QY 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220
 DB 1180 ATAGCAGATTTTGAACACAGAGAACACCCAGCAAAAGTAACTTGATGAAGAGCTGAT 1239
 QY 221 ValIleProProHisTrpProValArgThrValMetAsnThrIleGlnIleMetMet 240
 DB 1240 GTAATCTCTCACACACTCCAGTTAGAGCTGTATGAACATCAACATTAATATGATG 1299
 QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsn 260
 DB 1300 ATTTTAATTTGCAAGATGATCAACCTTCAGAAATCTATTTCTATTTTAAACAACTGC 1359
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
 DB 1360 ACAGTGAATCCAAAAGAAAGATATATCGAAAGAGTGAAGATATGATATCATCTTTAA 1419
 QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 DB 1420 GAGAAATTTGCTAAAGCTGTGGACAGGTTGTGTGGAATTTGATCAACAGATACAA 1479
 QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArg 320
 DB 1480 CTTGAGTTCGCTGTATATACCGAGTAAATGATCATCTTAATCAGAAAGAACGA 1539
 QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
 DB 1540 TTATTCATTTCAAAATTTTACCAAACTTCTGAATGACAAACATTTTCAATATGCTTTAT 1599
 QY 341 AlaCysAlaLeuGluValIleMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
 DB 1600 GCGTCCGCTCTTGAGGTTGTAATGCCACATATAGCAGAAATGATCTCAAAATCTTGAT 1659
 QY 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
 DB 1660 TCTGGAACAGATTTGTCTTCCATGATGATTCGAATGCTTAAATTTAAAGCCTTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
 DB 1720 TTTTAAACAAAGATCGAAGCTTTTATCAAGCAAGAGGCAACTTACAAAGAAATGATA 1779
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
 DB 1780 AAACATTAGAACGATGGAACATGCAATCATGATTCCTTGCATGCTCTCAGATTCA 1839
 QY 421 ProLeuPheAspLeuLeuLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440


```

Db 1840 CCTTATTTGATCTTATTAACAATCAAGACCGAAGAGGACCACTGATCACCCTTGAA 1899
OY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
Db 1900 TCTGCTGTCTCTTAACTTCCCTCCAGAAATTAATCAACAGCAGAGATGATGCTT 1959
OY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
Db 1960 TCTCTGTAAATCTCTAAAGAAAAGGTTCACTACGCGTGAATTAATCTACGCAAT 2019
OY 481 AlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
Db 2020 GCAGAGACACAAACCACTCAGCCTCCAGACCCCAACCACTTGAATTAATCTACCTCTT 2079
OY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyGlu 520
Db 2080 TCACGCTTTTAAAAAGCTGATCGGCTTAGCCTTATCTCCGCTTAAATACACTTTTGICAA 2139
OY 521 ArgLeuLeuSerGlnHisProGlnLeuGlnHisLeuTyrPheThrLeuPheGlnHisThr 540
Db 2140 CGCCTTCTGTCTGACACCCAGAAATAGAACATATCATCTGACCCCTTCCAGCAGCAC 2199
OY 541 LeuGlnAsnGlnTyrGlnLeuMetArgAspArgHisLeuAspGlnHisMetMetCysSer 560
Db 2200 CTGCGAATGAGCTATGAACATCATGAGAGACAGGCACTTGGACCAATTAATGATGTTCC 2259
OY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 580
Db 2260 ATGATGGCAATGCAAGAGAAAGAAATATAGACCTTAAATTAATGATGTAACACACA 2319
OY 581 TyrLysAspLeuProHisAlaValGlnGlnThrPheLysArgValLeuIleLysGlnGlu 600
Db 2320 TACAAAGATCTTCTCATGCTGTTCAAGAGACATCAACAGTGTGTTGATCAAGAAAGAG 2379
OY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
Db 2380 GAGTATGATTTCTATTAATGATTTCTAACTCGGTCTTATCGAAGACTGAAAACAAAT 2439
OY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
Db 2440 ATTTGCGATAGCTTCACACAGGCCGCCACCTGTGCACCAATGCTCACATTCCTCGA 2499
OY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlnGlyAsnIleTyrIleSer 660
Db 2500 AGCCTTACAGATTCTCTAGTCAACCTTAGCGATTCTCGAGGAGAACTTAATTTTCA 2559
OY 661 ProLeuLysSerProTyrLysIleSerGlnGlyLeuProThrProThrLysMetThrPro 680
Db 2560 CCCCTGAGAGCTCATATATAAAATTTTGAAGAGCTCTCCAAACACCAAAAAATGACTCCA 2619
OY 681 ArgSerArgIleLeuValSerIleGlyGlnSerPheGlyThrSerGlnLysPheGlnLys 700
Db 2620 AGATCAAGAAATCTTATGATCAATTTGGGAATCTTTGGGACTTTCGAGAAAGTCCAGAAA 2679
OY 701 IleAsnGlnMetValLysAsnSerAspArgValLeuLysArgSerAlaGlnGlySerAsn 720
Db 2680 ATAATCTGAGTGTATGTAACAGCAGCCGTGCTCAAAAAGAGGCTGGAAGAGCAAC 2739
OY 721 ProProLysProLeuLysLysLeuArgPheAspIleGlnGlySerAspGlnAlaAspGly 740
Db 2740 CCTCCTAAACACACGAAACAACTACGCTTGAATTTGAAGATGACAGATGAGACAGATGA 2799
OY 741 SerLysHisLeuProGlnGlyLysLeuPheGlnGlnLysLeuAlaGlnMetThrSerThr 760
Db 2800 AGTAAACATCTCCAGAGAGATCCAAATTCACAGCAAACTGGCAAAATGACTTCTACT 2859
OY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlnGlu 780
Db 2860 CGAAGCCGAATGCAAAAGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2919
OY 781 Lys 781

```

```

Db 2920 AAA 2922
RESULT 4
AAZ40287
ID AAZ40287 standard; cDNA; 2994 BP.
AC AAZ40287;
XX 24-FEB-2000 (first entry)
DE Wild type human retinoblastoma gene.
XX RB gene; human; retinoblastoma gene; mutation detection; immunoscreening;
XX retinoblastoma diagnosis; hereditary retinoblastoma; secondary cancer;
XX osteosarcoma; fibrosarcoma; glioblastoma; breast cancer;
XX tumorigenesis suppression; ss.
OS Homo sapiens.
XX
XX US5998134-A.
XX
XX 07-DEC-1999.
XX
XX 07-JUN-1995; 95US-0482627.
XX
XX 15-OCT-1987; 87US-0108748.
XX
XX 28-SEP-1992; 92US-0951947.
XX
XX (RBC ) UNIV CALIFORNIA.
XX
XX Lee EYP, Lee W;
XX WPI: 2000-052540/04.
XX
XX P-PSDB: AAY55060.
XX
XX Detecting retinoblastoma gene-cancer in mammals -
XX
XX Example 6; Fig 7; 34pp; English.
XX
XX This sequence represents the wild type human retinoblastoma gene.
XX The invention relates to a method of detecting a mutated retinoblastoma
XX (mRB) nucleic acid in mammals comprising hybridizing an isolated
XX full-length, wild-type RB (wtRB) cDNA probe to a cell sample and
XX detecting a mutated RB nucleic acid. The method is useful as a diagnostic
XX tool for diagnosing retinoblastoma. RB cDNA or genomic DNA are preferably
XX used as probes to determine the defect region of the mRB gene through
XX genomic DNA blotting analysis or using the method of restriction fragment
XX length polymorphism analysis to determine the diseased allele. Cloned RB
XX cDNA can be used to generate specific anti-RB protein (anti-ppRB110)
XX antibodies which are useful for immunoscreening of tissue biopsy. The
XX diagnostic method is particularly intended for use in screening
XX families with a history of hereditary retinoblastoma and for screening
XX their children. It may also be used in prophylactic and postnatal
XX screening and for the prediction of the development of secondary
XX cancer, such as, osteosarcoma, fibrosarcoma, glioblastoma, breast
XX cancer whether or not connected with retinoblastoma. The method is also
XX used in the suppression of tumorigenesis where the absent RB protein
XX ppRB110 will be provided through the molecular induction and gene
XX transplanting of the RB cDNA to the individual in need of ppRB110.
XX
XX Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0
XX Score: 4017.00
XX Percent Similarity: 100.00%
XX Best Local Similarity: 100.00%
XX Query Match: 100.00%
XX DB: 21
XX Gaps: 0
XX
XX US-09-026-459a-37 (1-781) x AAZ40287 (1-2994)
OY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGlnArg 20

```

Db	580	ATGTCAAGACCTGTGAACAAGTATGAGTATGTTTGTTCACCTCTTCACCAATTCGAAAG	639
Oy	21	ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer	40
Db	640	ACATGTGAACCTATATATTTATTCACCAACCCAGAGTGTGATCTACTGCAAAATATCT	699
Oy	41	AlaLeuValIleuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValIleGln	60
Db	700	GCAATTGGTCTCTAAAGATTTCCTGGATCATCTTTTATATAGCTAAAGGGAGAGTTTACA	759
Oy	61	MetGlnAspAspLeuValIleSerPheGlnLeuMetLeuCysValIleuAspTyrPheIle	80
Db	760	ATGGAAGATGATCTGTGATTCATTCATTCATTAATGCTATGTCCTGTGACTATTTTAT	819
Oy	81	LysLeuSerProPheMetLeuLysGluProLysTyrThrAlaValIleProIleAsn	100
Db	820	AAACTCTCACCTCCCATGTTCTCTAAAGAACCTATTAACACGCTGTATACCATATTAT	879
Oy	101	GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu	120
Db	880	GGTTTACCTCTGGAACCCAGCGAGGTCCAGAACAGAGTCCAGATGCAAAACACATCA	939
Oy	121	GluAsnAspThrArgIleGlnGluValLeuCysLysGluHisGlyCysAsnIleAspGln	140
Db	940	GAATAAGATACAAAGAAATATATGAGCTCTCTGTAAAGAAATGAAATATATAGATGAG	999
Oy	141	ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr	160
Db	1000	GTGAAAAATGTTTATTTCAAAAATTTATATACCTTTATGAATATCTCTTGAGCTTTGACA	1055
Oy	161	SerAspGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys	180
Db	1060	TCCTATGTGACTTCGAGAGTGGAAATCTTCTCAACGATACGAGAAATTTATCTTTAA	1113
Oy	181	AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer	200
Db	1120	AATTAAGATCTGTAGATGCAAGATATATTTTGTGATCATGATAAAACCTCTTCAGCTGATCT	1175
Oy	201	IleAspSerPheGlnThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn	220
Db	1180	ATAGACACGTTTGTGAACACAGAGACACCCAGCAAAAAGTAACTGTGATGAAGAGTCAAT	1235
Oy	221	ValIleProPheHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet	240
Db	1240	GTAATTCCTCCACACACTCCAGTTAGAGACTGTATGACATCATCCAAACATTTATGATG	1295
Oy	241	IleLeuAsnSerLysSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys	260
Db	1300	ATTTTAATATTCGCAAGATCATCACTTCAGAAAATCTGATTTCCATTTTAAACAATCTC	1355
Oy	261	ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys	280
Db	1360	ACATGCAATCTCAAAAGAAAGATTAAGTAAAGAGTAAAGATTAAGATTAAGTAAATCTTTAAA	1415
Oy	281	GluLysPheAlaLysAlaValAlaGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys	300
Db	1420	GAGAAATTTGCTTAAAGCTGTGTGGACAGAGTGTGTGCTGAAATTTGGATTCACGCAATCAAA	1475
Oy	301	LeuAlaValArgLeuTyrTyrArgValAlaMetGluSerMetLeuLysSerGluGluGluArg	320
Db	1480	CTTGAGATTCCTGCTTATTAACCGATTAAGAAATCCATTAATGATGAGAAAGAAAGCA	1535
Oy	321	IleuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu	340
Db	1540	TTTATCCATTCATAAATTTTACGAAACCTTCGAAAGCAACATTTTTCATATGCTTTATATG	1595
Oy	341	AlaArgAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp	360
Db	1600	GGGTGGCGCTCTTGAGATGTGATGTGGCCACTATATAGAGAGAAATCACTCCAAATCTTGAT	1655
Oy	361	SerGlyThrAspLeuSerPheProTrpIleLeuAsnValIleuAsnLeuLysAlaIleAsp	380

Dd	1660	TCGGAACAGATTTCCTTCCCATGGATTCGATAGTGCCTAATTAAAGCCTTGCAT	1719
Qy	381	PhetTytLyValIleGluSerPheIleIysAlaGluGlyAsnLeuThrArgGluMetIle	400
Dd	1720	TTTTACAAAGATATGAAAGATTATTAACAAAGCAAGAGCAACTGCACAAAGAAATGATA	1779
Qy	401	LyHisIleGluGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer	420
Dd	1780	AAACATTTTAGAACGATGTCGAAACATCGAATCATGGAATCCCTTGATGGCTCCAGATTCA	1839
Qy	421	ProLeuPheAspLeuIleIysGlnSerIysAspArgGluGlyProTrpAspHisLeuGlu	440
Dd	1840	CGTTTATTTGATCTTATTAATCAATCAAAAGACCGAAGACCAATGATCATCCTTGAA	1899
Qy	441	SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTrpLeu	460
Dd	1900	TCGCGTTGCCCTTAATCTTCCTCCAGAAATATCATCATCTGACGACGATATGATTCCTT	1959
Qy	461	SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn	480
Dd	1960	TCCTCGTAAAGATCCCAAAAAAAGGTGTCAACACGCGTGAATTTCTACTCGAAT	2019
Qy	481	AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu	500
Dd	2020	GCAAGACACAAAGCAACCTCGCCTCCACACCCAGAAAGCATTTGAATCTACTCTCTCT	2079
Qy	501	SerLeuPheTytLyValValTrpArgLeuAlaTrpLeuArgLeuAsnThrLysCysGlu	520
Dd	2080	TCACGTTTTATAAAAAGTGTATCGCTACGCTATCCGCTATCCGGTAAATATACCTTGTA	2139
Qy	521	ArgLeuLeuSerGlnHisProGluLeuGlnHisIleIleTrpThrLeuPheGlnHisThr	540
Dd	2140	CGCCTTCCTGTGACACCCAGATTGAAACATATCATCTGACCTTTTCCAGCACACC	2199
Qy	541	LeuGlnAsnGluTrpGlyLeuMetArgAspArgHisLeuAspGlnIleMetCysSer	560
Dd	2200	CTGAGAAAGATGATGAACTCATATGAGACAGGACATTTGGACCAAAATTATGACGTCTTC	2259
Qy	561	MetTytGlyIleCysValValLysAsnIleAspLeuLysPheLysIleIleValThrAla	580
Dd	2260	ATGATGCGCATATGCAAGTCAAGAAATATATGACCTTAATTCAAAATCTTGTACACGCA	2319
Qy	581	TyTrpAspLeuProHisAlaValAlaGluGluThrPheLysArgValLeuIleLysGluGlu	600
Dd	2320	TACAGAGATCTTCCCATGCTGTTCAGAGACATTCAAAACGTGTTGATCAACAAAGAG	2379
Qy	601	GluThrAspSerIleIleValPheTrpAsnSerValPheMetGlnArgLeuLysThrAsn	620
Dd	2380	GAGATGATTTCTATTAATGATTTCTATTAATCTTCGGCTTCTATGCAAGACAGCAAAACAT	2439
Qy	621	IleLeuGlnTrpAlaSerThrArgProTrpThrLeuSerProIleProHisIleProArg	640
Dd	2440	ATTTTGACATATGCTTCACACAGGCCCCCTACCTGTGCACAAATACATCAATTCCTGCA	2499
Qy	641	SerProTytLyAspPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrlIleSer	660
Dd	2500	AGCCCTTAACAATCTTCATAGTTCACCTTCAGGATCTCGAGGAGCAACATCTATTATCCA	2559
Qy	661	ProLeuLysSerProTytLyIleSerGlnGlyLeuProThrProThrLysMetThrPro	680
Dd	2560	CCCTGGAAGGTCATATTAATTTTCGAAAGGTCTGCCAACCAACAAAAAATGACTCCA	2619
Qy	681	ArgSerArgIleIleuValSerIleGlyGluSerPheGlyThrSerGlyLysPheGlnLys	700
Dd	2620	AGATCAAGAAATCTTGATTCATATTGGAGATCATCTCGGCACTCTGAAAGATTCACAA	2679
Qy	701	IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn	720
Dd	2680	ATTAATATCATATGATATGTAACAGGACCGGTGCTCAAAATAATGCTGAAAGAACAAAC	2739
Qy	721	ProProLysProLeuLysValLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly	740
Dd	2740	CGTCCTTAACCACTTAATAAAATCTACGCTTTCGATATTGGAAGAGATACATCTGAACGACATGCA	2799

QY	741	SettlySHisIeNpROcLYgluSerTyspNeGInGInTysIeAaIaGImeTtThrSerThr	760
Db	2800	AGTAAACATCTCCCGAGGAGTCCAAATTTCAGCGAANCTGCAGAAATGACTTCTACT	2859
OY	761	ArgTThrArgMeGInTysGInTysMeTAsnAPSerMeTAspThrTSerAsnTysGInGlu	780
Db	2860	CGAAGCAGAAATGCAAAAGCAGAAATAATGATGATGATACGATGATCTCAAAACAGAAAGG	2919
OY	781	Tys	781
Db	2920	AAA	2922
RESULT 5			
AAK90350			
ID	AAK90350	standard; cDNA; 2995 BP.	
XX	AAK90350;		
XX	27-SEP-1999	(first entry)	
XX	Human p110-RB retinoblastoma tumour suppressor encoding cDNA.		
KW	Human; p110-RB; retinoblastoma; tumour suppressor; gene therapy;		
KW	adenoviral protein IX; recombinant adenovirus expression vector;		
KW	cell cycle; p53; mitosis; cell death; apoptosis; thymidine kinase;		
KW	cancer; ss.		
XX	Homo sapiens.		
CS			
XX	Key	Location/Qualifiers	
FT	CDS	139..2825	
FT		/tag="a	
FT		/product="p110-RB"	
FT		/note="retinoblastoma tumour suppressor"	
XX	US95932210-A.		
PN	03-AUG-1999.		
PD			
XX	28-OCT-1997;	97US-0959638.	
XX	25-OCT-1994;	94US-0328673.	
PR	25-OCT-1993;	93US-0142669.	
PR	19-MAY-1994;	94US-0246006.	
PR	28-OCT-1997;	97US-0959638.	
XX	(CAN-) CANJ1 INC.		
XX	Gregory RJ, Maneval DC, Wills KM,		
XX	WPI: 1999-443568/37.		
DR	P-PSDB; AMI24471.		
XX	Recombinant adenoviral vectors useful for gene therapy of cancer,		
XX	especially p53 deficient tumours		
PS	Disclosure; Fig 3; 50pp; English.		
XX	The present invention describes a composition comprising a recombinant		
XX	adenovirus expression vector, where the vector has an insert of		
CC	exogenous DNA comprising a gene encoding a foreign protein and		
CC	adenovirus DNA in which all of the coding sequences of E1a, E1b, and		
CC	protein IX, and part of E3 are deleted. The vectors are useful in gene		
CC	therapy treatment of cancer, especially for treating p53 deficient		
CC	tumours. The vector enables safer and more efficient gene therapy of		
CC	cancer. The present sequence encodes human p110-RB retinoblastoma		
CC	tumour suppressor which can be used as the foreign gene in the above		
XX	Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;		
SQ	Alignment Scores:		

Db 2320 TACAAGGATCTTCCTCATGCTGTCAGAGACATCAACGCTTTTGATCAAGAAGAG 2379
 QY 601 GUYTAApSerllelleValPheTYrAsnSerValPheMetClnArgLeuAspThrAsn 620
 Db 2380 GAGTATGATTCATATATAGTATTCATATACCTCGTCTTATGAGAGACTGAAACAAAT 2439
 QY 621 lleAaGlnTYrAlaSerThrArgProPheThrLeuSerProIleProHisIleProArg 640
 Db 2440 ATTTCGAGTATGCTTCACAGAGCCCTTACTTGTACACAAATACCTACATTCCTCGA 2499
 QY 641 SerProTYrLysPheProSerSerProLeuAlaIleProGlyGlyAsnIleTYrIleSer 660
 Db 2500 ACCCTTCAGAGTTTCCTAGTTCACCTTCAGAGATTCCTGAGAGAAACATCTATATTTC 2559
 QY 661 ProLeuLysSerProTYrLysIleSerGlyLysProThrProThrLysMetThrPro 680
 Db 2560 CCCCTGAGAGATCCATATATAATTTGAGAGAGCTGCAACACCAACAAATATGACTCCA 2619
 QY 681 ArgSerArgIleLeuValSerIleGlyLysPheGlyThrSerGlyLysPheGlnLys 700
 Db 2620 AGATCAAGATCTTATGATTCATATGATGATGAGATTCGGGACTTCGAGAGATTCAGAAA 2679
 QY 701 lleAaGlnMetValCysAsnSerAspArgValleuLysArgSerAlaGlyLysSerAsn 720
 Db 2680 ATAAATCAGATGATGATTAACAGAGCAGCTGCTCAAAAAGATGCTGAGAGAGCAAC 2739
 QY 721 PropolLysProLeuLysLysLeuArgPheAspIleGlyLysSerAspGlnAlaAspGly 740
 Db 2740 CCTCTAAACCACTGTAATAAACTACGCTTGTATTTGAAAGATCAGATTAACCAAGATGGA 2799
 QY 741 SerLysHisLeuProGlyLysLysPheGlnGlnLysLeuAlaIleMetThrSerThr 760
 Db 2800 AGTAAACATCTCCAGAGAGACTCCAAATTCACAGAACTGCGAAGAAATGACTTCTACT 2859
 QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlnGln 780
 Db 2860 CGAAGACAGATGCAAAAGCAAAATATGATGATGATGATGATGATGATGATGATGATG 2919
 QY 781 Lys 781
 Db 2920 AAA 2922
 RESULT 7
 AAH25755
 ID AAH25755 standard; DNA; 2995 BP.
 XX
 AC AAH25755;
 XX 14-AUG-2001 (first entry)
 Retinoblastoma tumour suppressor gene.
 XX Retinoblastoma tumour suppressor protein; Rb; p53; cancer;
 KW adenoviral vector; gene therapy; thymidine kinase; ds.
 XX
 OS Unidentified.
 XX
 PN US2001006629-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 24-NOV-1999; 99US-0449113.
 XX
 PR 25-OCT-1994; 94US-0328673.
 PR 25-OCT-1993; 93US-0142669.
 PR 19-MAY-1994; 94US-0246006.
 XX
 PA (GREG/) GREGORY R J.
 PA (WILL/) WILLS K N.
 PA (MANE/) MANEVAL D C.
 XX
 PI Gregory RJ, Wills KN, Maneval DC;
 XX

DR WPI: 2001-397210/42.
 DR P-PSDB: AAB98945.
 XX
 PT Recombinant adenovirus expression vector comprising a partial or total
 PT deletion of a protein IX DNA and a gene encoding a foreign protein e.g.
 PT suicide protein, useful for inhibiting or reducing the proliferation of
 PT a tumour e.g. brain tumour -
 XX
 PS Disclosure: Fig 3; 39pp; English.
 XX
 CC The present invention describes an adenoviral expression vector
 CC comprising a deletion in the protein IX gene and a gene encoding a
 CC foreign protein. This vector can be used in gene therapy, particularly to
 CC introduce tumour suppressor genes into cancerous cells. Genes which may
 CC be used include p53, thymidine kinase and retinoblastoma tumour
 CC suppressor gene (Rb). The present sequence is the retinoblastoma tumour
 CC suppressor gene.
 XX
 SO Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other:
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-026-459a-37 (1-781) x AAH25755 (1-2995)
 QY 1 MetSerArgLeuLeuLysLysTYrAspValleuPheAlaLeuPheSerLysLeuGlnArg 20
 Db 580 AGTCAAGACAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 639
 QY 21 ThrGysGluLeuIleTYrLeuThrGlnProSerSerSerIleSerThrGlnLeuSer 40
 Db 640 AGATGAGACTTATATATTTGACCAACCCAGAGCTTCATATCTACATATATATATAT 699
 QY 41 AlaLeuValleuLysValSerTPIleThrPheLeuLeuAlaLysGlyLysValleuGln 60
 Db 700 GCATTTGGTGTAAAGATTTCTTGATGATCACAATTTTATAGCTTAAGCGGAGATATTA 759
 QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValleuAspTYrPheIle 80
 Db 760 ATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
 QY 81 LysLeuSerProProMetLeuLeuLysGlnProTYrLysThrAlaValIleProIleAsn 100
 Db 820 AAAGCTCACCTCCCATGTTGCTCAAGAAACATATATAACAGCTGTATATACCATTTAT 879
 QY 101 GlySerProArgTYrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 Db 880 GGTTCACCTCGAACACCCAGCGAGGTGACAGACAGAGAGTGCAGATGACAAACAACTA 939
 QY 121 GluAsnAspThrArgIleIleGlyValleuLysGlnLysGlnLysAsnIleAspGln 140
 Db 940 GAAATGATACAGATATATGAAATGCTCTGTAAAGAACATGAATGATATATAGATAG 999
 QY 141 ValLysAsnValTYrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
 Db 1000 GTGAATAATGTTTATTTCAAAAATTTTATACCTTTATGAAATTCCTTGACTGTACA 1059
 QY 161 SerAsnGlyLeuProGlyValGlyAsnLeuSerLysArgTYrGlnGlnIleTYrLeuLys 180
 Db 1060 TCTAATGACCTTCAGAGAGTTGAAATCTTTCTTAACGATACAGAGAAATTTATCTTAA 1119
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 Db 1120 AATTAAGATCTAGATGCAAGATTTATTTTGTGATCATGATTAACCTCTCAGACTGATCT 1179
 QY 201 IleAspSerPheGluThrGlnArgTYrProArgLysSerAsnLeuAspGlnValAsn 220
 Db 1180 ATAGACATTTTGAAGACAGAGAACACAGAAATATGATGATGATGATGATGATGATGAT 1239

XX 25-OCT-1993: 93US-0142669.
 PR 19-MAY-1994: 94US-0233777.
 XX
 XX (CANU-) CANUI INC.
 XX
 PI Gregory RJ, Wills KN, Maneval DC;
 XX
 DR WPI: 2001-289633/30.
 DR P-PSDB: AAE00689.

XX New recombinant adenovirus expression vector having a gene encoding for
 PI a foreign protein and a partial or total deletion of the adenoviral
 PT protein IX DNA, useful in gene therapy for treating or reducing
 PT hyperproliferative cells -
 XX
 XX
 PS Disclosure: Fig 3; 4pp; English.

XX The present cDNA sequence encodes retinoblastoma (RB) tumour suppressor
 CC protein, designated as p110RB.
 CC The invention relates to a recombinant adenovirus expression vector
 CC characterized by the partial or total deletion of the adenoviral protein
 CC IX DNA beginning at nucleotides 357 or 360 and ending at 4020-4050, and
 CC having a gene encoding a foreign protein such as tumour suppressor
 CC protein, p110RB (retinoblastoma) and p53. Adenovirus vector is used
 CC for screening tumour suppressor genes useful in gene therapy. The vector
 CC is particularly useful for treating or reducing hyperproliferative cell
 CC disorders such as thyroid hyperplasia, Grave's disease, psoriasis,
 CC benign prostatic hypertrophy, Li-Fraumeni syndrome, cancers specifically
 CC hepatocellular carcinoma, neoplasms, leukaemias, lymphomas, etc. to
 CC inhibit tumour proliferation or to ameliorate particular related
 CC pathology such as sickle cell anaemia and Tay-Sachs disease. The vector
 CC is also useful for the safe recombinant production of diagnostic and
 CC therapeutic polypeptides and proteins.
 XX

SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2995
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-026-459A-37 (1-781) x AAD04474 (1-2995)

QY 1 MetSerArgLeuIeuLysTyrAspValIleupheAlaIleupheSerLysLeuGluArg 20
 |||||||
 DB 580 ATGTCAAGACGTGTGAAGAAAGATGATGATGTTGTGGACCTCTTCAGCAAAATGGAAAG 639
 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerLysSerThrGluIleAsnSer 40
 |||||||
 DB 640 ACATGTGAAGCTTATATATTTGGACCAACCCAGAGTGCATGTACAGTAATTAATTTCT 699
 QY 41 AlaLeuValIleuLysValSerTPIIleThrPheLeuLeuAlaLysGluValLeuGln 60
 |||||||
 DB 700 GCATTGGTGGTAAAAAGTTCTTGATGCACATTTTATTAAGCAAAAGGGAAGTATTACA 759
 QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
 |||||||
 DB 760 ATGGAAGTGAATGCTGGATTTTCATTCAGTAAATGCTATGTCCTTGACATATTATAT 819
 QY 81 LysLeuSerProMetLeuLeuLysGluProTyrIleThrAlaValIleProIleAsn 100
 |||||||
 DB 820 AAACCTCCACCTCCCATGTTGCTCAAAAGAACCATATAAAGCGCTGTAATCCATTAAAT 879
 QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 |||||||
 DB 880 GGTTCACCTCGAACCCAGCCAGGTGCAGACAGAGGTGCAGGATAGCAAAACACTA 939
 QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu 140
 |||||||

DB 940 GAAATGATACAGAATATTGAAAGTCTCTGTAAAAAGACATGATGTAATATAGATGAG 999
 QY 141 ValLysAsnValIleTyrPheLysAsnPhaIleProPheMetLeuSerLeuGluValIleThr 160
 |||||||
 DB 1000 GTGAATAAATGTTATTTCACAAAATTTTATATACCTTTTATGAAATCTCTTGACCTGTAAACA 1059
 QY 161 SerAsnGlyLeuProGlyValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
 |||||||
 DB 1060 TCTAATGACCTTCAGAGGTGAAGAAATCTTCTCAACGATACGAAAGAAATTTATCTTAA 1119
 QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
 |||||||
 DB 1120 AATAAAGATCTAGATGCAAGATTTATTTGGATCATGATATAAAGCTTCAGCATGATTC 1179
 QY 201 IleAspSerPheGlnThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn 220
 |||||||
 DB 1180 ATGACAGCTTTGAAACACAGACAGACACCAAGAAAAGTAAACCTTGATGAAAGGTGAT 1239
 QY 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet 240
 |||||||
 DB 1240 GTAATTCCTCCACACACTCCAGATGAGACGTGATGAAACACTATCCAAATTAATGATG 1299
 QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
 |||||||
 DB 1300 ATTTTAAATTCAGCAAGATGATCAACCTTGAGAAATCTGATTTCTATTTTAAACAATCG 1359
 QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
 |||||||
 DB 1360 ACAGTGAATCCAAAGAAAGATGATCTGAAGAGTGAAGATGATGATGATCTCTTAA 1419
 QY 281 GluLysPheAlaLysAlaValAlaGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
 |||||||
 DB 1420 GAGAAATTTGGCTAAAGCTGTGGGACAGGGTGTGTCGAAATTTGGATGCACAGCGATACAA 1479
 QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
 |||||||
 DB 1480 CTGGAGTTCGCTGTGTATTAACGAGTATGGAATTCATGCTTAATCAGAAAGAAACGA 1539
 QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
 |||||||
 DB 1540 TTATCCATTTCAAAATTTTATGCAAACTTCTGAATGACAACTTTTCAATATCTCTTATG 1599
 QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
 |||||||
 DB 1600 GCGTGGCTCTTGAGGTGTGTAATGGCCATATAGCAGAAATCTTCACAAATCTTGAT 1659
 QY 361 SerGlyThrAspLeuSerPheProThrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
 |||||||
 DB 1660 TCTGAAACAGATTTGTCTTTCCATGATTTCTGATGTCTTAATTTAAAGCCTTGAT 1719
 QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
 |||||||
 DB 1720 TTTTACAAAGTGAATCGAAAGTTTATCAAAAGCAGAAAGCAACTTGACAAAGAAATGATA 1779
 QY 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaIlePheLeuSerAspSer 420
 |||||||
 DB 1780 AAACATTTAGAACATGTGAACATCGAATCATGGAATCCCTTGCAATGCCCTTCGATTTCA 1839
 QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
 |||||||
 DB 1840 CCTTATTTGATCTTATTAACAATCAAAAGACCGGAGGAGCAACGATGACACTTGAA 1899
 QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
 |||||||
 DB 1900 TCGGCTGTGCTCTTAATCTTCCTCCAGAAATTAATCAACATCGCAGCATATGTATCTT 1959
 QY 461 SerProValArgSerProLysLysGluIleSerThrThrArgValAsnSerThrAlaAsn 480
 |||||||
 DB 1960 TCTCCTGTAAAGTCTCCAAAGAAAAAGGTTCAACTACCGGTGTAATTTCTACTGCAAT 2019
 QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
 |||||||
 DB 2020 GCAGAGACACAAAGCAACTCAGCTTCACAGACCCAGAAAGCCATGTGAATTTACTCTCTT 2079

OY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
 |||||||
 Db 2080 TCACGTCTTTATATAAAGTGTATCGGTACCTATCTCCGGCAATAATATACACTTGTGAA 2139
 OY 521 ArgLeuLeuSerGlnHisProGluLeuGlnHisIleIleIleProThrLeuPheGlnHisIle 540
 |||||||
 Db 2140 CGCCTTCTGTCTGAGCACCACCAATATACATCATCTGAGACCTTTTCCAGCACACC 2199
 OY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
 |||||||
 Db 2200 CTCACAAATGAGTATGCAATCATGAGAGACGCAATTTGGACCAATATATGATGCTTCC 2259
 OY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValIleTrpAla 580
 |||||||
 Db 2260 ATGTATGGCATATGCAAAATGAAATATAGACCTTAATTCAAATATCATGTATGACGCA 2319
 OY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValIleuIleLysGluGlu 600
 |||||||
 Db 2320 TACAGAGATCTTCATCTCATGCTGAGAGACATTCAAACGCTTTTGATCAAAAGAGAG 2379
 OY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysTrpAsn 620
 |||||||
 Db 2380 GAGATGATTTAT 2439
 OY 621 IleLeuGlnTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArg 640
 |||||||
 Db 2440 ATTTTGAGATGCTTCCACGAGCCCTTACCTGTACCAATATCTCATCTTCCATCGA 2499
 OY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer 660
 |||||||
 Db 2500 AGCCCTTACAAAGTTCCTAGTTCACCCCTTACGAGATTCCTGAGGAGAACATCTATTTTCA 2559
 OY 661 ProLeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrPro 680
 |||||||
 Db 2560 CCCCTGAGAGTCCATATATAATTTTCAAGAGTCTGCCAACACCAACAAAAATGACCTCCA 2619
 OY 681 ArgSerArgIleLeuValSerIleLeuValSerPheGlnThrSerGluLysPheGlnLys 700
 |||||||
 Db 2620 AGATCAAGAACTTACTATCAATATGTAATCATTCGGGACTTCTGAGAGTTCCAGAA 2679
 OY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
 |||||||
 Db 2680 ATAAATCAGATGCTATGTATTAACAGCCGCTGCTCAAAATAAGTCTGAAAGACCAAC 2739
 OY 721 ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly 740
 |||||||
 Db 2740 CCTCTTAACCACTGAAAAAACTACGCTTTGATATTGAAGATATGATGAAGCATGATGA 2799
 OY 741 SerLysHisLeuProGlyLysLeuSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
 |||||||
 Db 2800 AGTAAACATCTCCAGAGAGTCCAAATTTTCAGCGAAGAACTGCGCAAAATGACTTCTACT 2859
 OY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGly 780
 |||||||
 Db 2860 CGAACACGATGCAAAAGACGAATGATGTATGACATGATCTCTCAAAACGAAGAGAG 2919
 OY 781 Lys 781
 ||||
 Db 2920 AAA 2922
 RESULT 9
 ABL50904 ID ABL50904 standard: cDNA: 2995 BP.
 XX
 AC ABL50904;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Retinoblastoma tumour suppressor protein p110-RB encoding cDNA.
 XX
 KW Retinoblastoma; tumour suppressor protein; p110-RB; cell cycle; p53;
 RB; mitosis; cell death; adenoviral protein IX; gene therapy; cytostatic;

KW adenovirus expression vector; tumour; non-small cell lung cancer;
 KW small cell lung cancer; hepatocarcinoma; hepatocellular carcinoma;
 KW melanoma; retinoblastoma; colorectal carcinoma; sarcoma; Wilms' tumour;
 KW astrocytoma; glioblastoma; neuroblastoma; ovarian carcinoma;
 KW osteosarcoma; renal cancer; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 139..2925
 FT /tag= a
 FT /product= "retinoblastoma tumour suppressor protein"
 PN US2001016192-A1.
 PD 23-AUG-2001.
 XX
 PF 28-OCT-1997; 97US-0958570.
 XX
 PR 25-OCT-1994; 94US-0328673.
 PR 25-OCT-1993; 93US-0142669.
 PR 26-APR-1994; 94US-0233777.
 XX
 PA (GREG/) GREGORY R J.
 PA (WILL/) WILLS R N.
 PA (MANE/) MANEVAL D C.
 XX
 PT Gregory RJ, Wills KN, Maneval DC;
 XX
 DR WPI: 2001-53532/59.
 DR P-PSDB: ABB07055.
 XX
 PT New recombinant adenoviral vector comprising a partial or total
 PT deletion of a protein IX DNA and a gene encoding a foreign protein,
 PT useful in gene therapy, particularly for treating or suppressing
 PT proliferation of a tumor -
 XX
 PS Disclosure; Fig 3; 37pp; English.
 XX
 CC The present invention describes a recombinant adenovirus expression
 CC vector, which comprises a partial or total deletion of a protein IX DNA
 CC and a gene encoding a foreign protein. The recombinant adenovirus vector
 CC can have cytostatic activity and be used in gene therapy. The recombinant
 CC adenovirus expression vector is particularly useful for treating or
 CC suppressing proliferation of a tumour, e.g. non-small cell lung cancer,
 CC small cell lung cancer, hepatocarcinoma or hepatocellular carcinoma,
 CC melanoma, retinoblastoma, breast tumour, colorectal carcinoma, sarcoma,
 CC prostate tumour, bladder tumour, tumour of the reticuloendothelial
 CC tissues, Wilms' tumour, astrocytoma, glioblastoma, neuroblastoma,
 CC ovarian carcinoma, osteosarcoma or renal cancer. The present sequence
 CC encodes the retinoblastoma tumour suppressor protein p110-RB, which is
 CC given in the exemplification of the present invention.
 XX
 SO Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 23 Gaps: 0
 US-09-026-459A-37 (1-781) x ABL50904 (1-2995)
 OY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
 |||||||
 Db 580 ATGTCAAGAGCTGTGAGAGAGTATGTTTTCACACTTTCAGCAATTTGGAAAG 639
 OY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerIleSerThrGluLeuAsnSer 40
 |||||||
 Db 640 ACATGTGACATATATATTTTGCACACACCCAGCTTCGATATCTCATGATAAATAATCT 699

QY	41	AlaLeuValLeuLysValSerTrpLleThrPheLeuLeuAlaLysGlyValLeuGln	60
Db	700	GCATTTGGTGTCTAAAGTTTCTTGATCAACATTTTATTAAGCTAAAGGGAGCTATTACAA	759
QY	61	MetGlnAspAspLeuValLleSerPheGlnLeuMetLeuCysValLeuAspLysPheLle	80
Db	760	ATGGAAGATGATCTGGTGGATTCATTTCAGTTTAAGCTAATGATGTGCTGACATATTTATTT	819
QY	81	LysLeuSerProProMetLeuLeuLysGluProLysTrpLysThrValAlaLleProLleAsn	100
Db	820	AAACTCTCACTCCCATCTGGTGTCTCAAGAAACCTATTAACAGCTGTATTACCCATATAT	879
QY	101	GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgLleAlaLysGlnLeu	120
Db	880	GGTTCACCTCCGAAACCCAGGCGAGGTCAAGAACAGATGTCAGAGATGAACAAACACTA	939
QY	121	GlnAsnAspThrArgLleLleGlyValLeuLysGlyLysGlnHisGlyCysAsnLleAspL	140
Db	940	GAATAATGATACAAAGATTTATGAAGTTCCTGTAAAGAACATGAATATATATATATAGTAG	999
QY	141	ValLysAsnValLysPheLysAsnPheLleProPheMetAsnSerLeuGlyLeuValThr	160
Db	1000	GTGAAAAATGTTTATTTCCTCAAAAATTTTATACCTTTATGATATCTCTGGACCTGTACA	1059
QY	161	SerAsnGlyLeuProGluValGlnAsnLeuSerLysArgTyrGluGlnLleTyrLeuLys	180
Db	1060	TCTTAATGACATCCAGAGGTGTGAATCTTTTAAACATACGAAAGAAATTTATCTCTAAA	1119
QY	181	AsnLysAspLeuAspAlaArgLeuPheLeuAsnAspLysAspLysThrLeuGlnThrAspSer	200
Db	1120	AATAAAGATCTGATCGATCGAACGATTATTTTTGGATCATGATGATTAACCTCTCCGACTGATCT	1179
QY	201	LleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsn	220
Db	1180	ATGAGACAGTTTGAACACACAGAACACACACCAAAAATTAACCTTGTATGAAAGGTGAT	1239
QY	221	ValLleProProHisThrProValArgThrValMetAsnThrLleGlnLeuMetMet	240
Db	1240	GTATATTCCCTCACACACTCCAGTTAGAGCTGTATGAACACTATCCACAAATTAATGATG	1299
QY	241	LleLeuAsnSerAlaSerAspGlnProSerGluValAsnLleLysSerTyrPheAsnGly	260
Db	1300	ATTTTAAATTCAGCAAGATGATCAACCTTGAGAAATCTGATTCCTATTTTAAACAACGCC	1359
QY	261	ThrValAsnProLysGluSerLleLeuLysArgValLysAspLleGlyTyrLlePheLys	280
Db	1360	ACAGTAAATCCAAAAGAAAGATATCTGAAAAGAAAGGAGATATAGGATATCAATCTTTAAA	1419
QY	281	GluLysPheAlaLysAlaValGlyGlnGlyCysValGluLleGlySerGlnArgTyrLys	300
Db	1420	GAGAAATTTGCTTAAGCTGTGGGACAGGGGTGTGTGCAAAATTTGATGCACAGGATCAAA	1479
QY	301	LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluValArg	320
Db	1480	CTTGGAGTTTCGGTGTATTTACCCGATATGAGATCCATGCTTAATATCAGAAAGAAAGACA	1539
QY	321	LeuSerLleGlnAsnPheSerLysLeuLeuAsnAspAsnLlePheHisMetSerLeuLeu	340
Db	1540	TTATTCATTCACAAATTTTACGAAACTCTGATATGACACATTTTTCATATGCTTTATATG	1599
QY	341	AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp	360
Db	1600	GCGGTGGCTCTTGAGGTGTGTAATGGCCACATATACCAAAATGATATCTCCAGAAATCTGAT	1659
QY	361	SerGlyThrAspLeuSerPheProTrpLleLeuAsnValLeuAsnLeuLysAlaPheAsp	380
Db	1660	TCTGGAAACGAATTTGCTTTCCCTCCATGGATTCGATATGCTTAATTTAAAGCCTTTGAT	1719
QY	381	PheTyrLysValLleGluSerPheLleLysAlaGluLysValLeuLeuThrArgGluMetLle	400
Db	1720	TTTTTACAAAGTATCGAAAGTTTATATCAAAAGCAAGGCATCTGTACAAAGAAATGATA	1779
QY	401	LysHisLeuGluValArgCysGluHisArgLleMetGluSerLeuAlaTrpLeuSerAspSer	420

Db	1780	AAACATTTCAGAACGATGGCAACATCGAATCATGGAATCCCTTGATCGCTTCAGATTCGA	1839
Qy	421	ProLeuPheAspLeuIleValGlnSerLysAspArgGluGlyProThrAspHisLeuGlu	440
Db	1840	CCATTATTTGATCTTAATTAAACAAATCAAAAGCAGGAGGACCACTGATCACTCTGAA	1899
Qy	441	SerLysCysProLeuAsnLeuProLeuGlnAsnAsnHisThrIleAlaAspMetLysLeu	460
Db	1900	TCGCTGTGCTCCCTTAACCTTCCTCCCAAAATATACACTGCAAGCATGATAGTATCTT	1955
Qy	461	SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrIleAsn	480
Db	1960	TCCTCGTTAAGATCTCCAAAAAGAAAGGCTTCACAGCGCTGTAATTTACTCGCAAT	2019
Qy	481	AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu	500
Db	2020	GCAAGACACAAAGCAACCTCAAGCTTCACAGCCCAAGCCAACTGAATATCTACTCTCT	2079
Qy	501	SerLeuPheLysLysValLysValLysArgLeuAlaLysLysArgLeuAsnThrLeuCysGlu	520
Db	2080	TCACGTGTTTATAAAAAGATGATCGGCTAGCGCTATCCGGCTAAATTAACCTTTGAA	2139
Qy	521	ArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIleThrPheLeuPheGlnHisThr	540
Db	2140	CGCTTCCTGCTGAGCAACCCAGAAATTTGAACATATCATGTGACCTTTTCCAGCAAC	2199
Qy	541	LeuGlnAsnGluLysGluLeuMetLysAspArgHisLysLeuAspGlnIleMetMetCysSer	560
Db	2200	CTCGACAGATCACATCAACCTCATGACAGACAGCATTTGGACCAAAATTAAGATGTCTCC	2259
Qy	561	MetLysGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla	580
Db	2260	ATGATAGCGATATGCAAGATGAAGATATGAGCTTAAATTCATAATCATTTGTAACGCA	2319
Qy	581	TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluLys	600
Db	2320	TACAGAGCTTCCTCCATGCTGTTCCAGAGACATCTCAAAACGTGTTTGATCAAAAGAGAG	2379
Qy	601	GluLysAspSerIleIleValPheTyrAsnSerValPheMetGlnAspLeuLysThrAsn	620
Db	2380	GAGATAGATTCATTAATGATGATCTTAATACCTGCTTCATGACAGACATGAAACAAAT	2439
Qy	621	IleLeuGlnTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArg	640
Db	2440	ATTTTGAGATGACCTCCACAGGCCCCCTTACCTTCCACAAATATCCCATATCTCTCA	2499
Qy	641	SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer	660
Db	2500	AGCCCTTACAGATTCCTAGTTTCAACCTTACGGATTCCTGGAGGGAACATCTAATTTCA	2559
Qy	661	ProLeuLysSerProTyrLysIleSerGlnGlyLeuProThrProThrLysMetThrPro	680
Db	2560	CCCCGAGAGCTCCAAATTAATTTCAAGAAAGCTCCCAACCAACCAAAAAATGACTCCA	2619
Qy	681	ArgSerArgIleLeuValSerIleGlyGlnSerPheGlyThrSerGluLysPheGlnLys	700
Db	2620	AGATCAAGATCTCTAGTATCAATGATGATCATTTCCGGGACTTCCGAAAGTTCCAGAAA	2679
Qy	701	IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn	720
Db	2680	ATAATTCATGATGATATGTAACAGGACCGGTCTCTAAAACGAAGCTCCAGAGCAACAC	2739
Qy	721	ProProLysProLeuLysLysLeuArgPheAsnIleGluLysSerAspGluAlaAspGly	740
Db	2740	CCCTCTTAACACATGAAAAAACTACGCTTGAATTAAGAGCATGAGATGAACAGATGCA	2799
Qy	741	SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr	760
Db	2800	AGTAAACATCTCCACGAGAGTCCAAATTTCCACAGAAACTGCGAGAAATGACTCTACT	2855
Qy	761	ArgThrArgMetClnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluLys	780

Db 2860 CGAACGATGCAAGCAAGCAAAATGATGTAGCATGATGATACCTCAACAGAGAGAG 2919

Oy 781 Lys 781

Db 2920 AAA 2922

RESULT 10

AAV58445

AAV58445

AAV58445

02-DEC-1998 (first entry)

Modified retinoblastoma tumour suppressor gene.

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

Oy 41 AlaleuValleuValserTriethrPheLeuAlaLysGluValLeuGln 60

Db 127 GCATTGCTGCTAAAGAGTTCTTGTGATCACAATTTATATGCTAAAGGAGATTTACAA 186

Oy 61 MetGluAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80

Db 187 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246

Oy 81 LysLeuSerProPheMetLeuLeuLysGluProLysTyrAlaValIleProIleAsn 100

Db 247 AAACCTCACCCTCCATGCTGCTCAAGAAACCATATTAACAGCTTATACCATTAAT 306

Oy 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120

Db 307 GGTTCACCTGCAACACCCAGCGATGCAAGACAGAGAGTGCAGATGCAAAACACTA 366

Oy 121 GluAsnAspThrArgIleIleGluValIleCysLysGlnIleGlyCysAspIleAspGlu 140

Db 367 GAAATGATACAAATATATGAAAGTTCTGTAAAGAACATGATATATATGATGAG 426

Oy 141 ValLysAsnValIlyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160

Db 427 GTGAAAAATGTTATTTTCAAAAAATTTTATACCTTTATGAAATTCCTTGACCTGTACA 486

Oy 161 SerAsnGlyLeuProGluValIleGluAsnLeuSerLysArgTyrGluIleTyrLeuLys 180

Db 487 TCTATGAGACTTCCAGAGTTGAAATCTTTCAACATGATGAAAGAAATTTATCTTAA 546

Oy 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspLysAspLysThrLeuGlnThrAspSer 200

Db 547 AATTAAGATCTGATGCAAGATATTTTGGATGATGATGATGATGATGATGATGATGATG 606

Oy 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluValAsn 220

Db 607 ATAGACACTTTTGAACACAGACAGACACACGAAAGATTAACCTTGATGAGAGGTGAT 666

Oy 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMet 240

Db 667 GTAATTCCTCCACACTCCAGTGTAGAGCTGTATGAAACACTATCCAAACATTAATGATG 726

Oy 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsn 260

Db 727 ATTTAAATTCAGCAAGATGATCAACCTTCGAAATCTGATTTCTATTTAAACACTGC 786

Oy 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280

Db 787 ACAGTGAATCCAAAGAAAGATATCTGAAAGAGTGAAGATATAGCATACATCTTTAA 846

Oy 281 GluLysPheAlaLysAlaValIleGlyGlnGlyCysValIleGlySerGlnArgTyrLys 300

Db 847 GAGAAATTTGCTAAAGCTGTGGACAGGGTGTGTGAAATTTGATACACGAGATACAA 906

Oy 301 LeuGlyValArgLeuTyrTyrArgValIleMetGluSerMetLeuLysSerGluGlnLys 320

Db 907 CTTGGAGTTCCTGCTGTATTCACGAGTATGATGATGATGATGATGATGATGATGATG 966

Oy 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340

Db 967 TTATCCATTTCAAAATTTTACCAAACTTGTGAAGACAACTTTTCAATATGCTTTATG 1026

Oy 341 AlaCysAlaLeuGluValIleMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360

Db 1027 GCGTCGCTCTTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086

Oy 361 SerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380

Db 1087 TCTGCAACAGATTTGTCTTCCATGATCTGAAAGTCTTAATTTAAAGCCCTTTGAT 1146

Oy 381 PheTyrLysValIleGluSerPheIleLysAlaGlyLysLeuThrArgGluMetIle 400

Db 1147 TTTTCAAAAGATCGAAAGATTTATCAAGCAAGACCACTTGACCAAGAAATGATA 1206

Oy 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTyrLeuSerAspSer 420

Db	1207	AAACATTGGAACGATGGGAACATCATCATGGAATCCCTTGATGGCTCAGATTC	1266
Qy	421	ProLeuPhaSpLeuLLeuYsGInSerLySAsPaYgLuYpProPhaSPHsLeuGlu	440
Db	1267	CTTTATTGGACTTATTAAACATCAAGAGCCGAGAGGACCACTGATCAGCTGGA	1326
Qy	441	SeRiLaCySpProLeuAaLeuProLeuGInAaSaAnHsThRaLaLaSpMeThyLeu	460
Db	1327	TGCGTGGCCCTTAACTCTTCTCCGAAATATCATCTGCAGCAGATATGTTCT	1386
Qy	461	SePProVaLaYgSerProLySLeuYgLySerThThRaYLaSaSerThRaLaS	480
Db	1387	TGTCGGVAAAGTCTCCAAAGAAAAAGGTCTAACTACGCGTAAATTTCTACGAAAT	1446
Qy	481	AlaGluThRGlNaLaThSerLaPheGInThRGlNuYsProLeuYsSerThSerLeu	500
Db	1447	GCAGAGACCAAGCAACCTCAGCCCTCCAGACCCAGAAAGCATTGAAATCTACTCTCT	1506
Qy	501	SeRLeuPhaTyLeuYsVaLYaYzArgLeuLaLaYrLeuLaYgLeuSaAnThRLeuCYsGlu	520
Db	1507	TCACGTGTTTAAAAAAGGTATACGCGTATCCGCTATCCCGGTAAATACACTGTGTGA	1566
Qy	521	ArgLeuLeuSerGInHsProGluLeuGInHsLLeIeTPrThRaLeuPheGInHsThR	540
Db	1567	CGCCTTCTGTGAGCACCCGAAATTAAGAAATATCATCTGGACCTTTCCAGCGACAC	1626
Qy	541	LeuGInAspGluThYsGluLeuMeTaYgAsPaYgHsLLeuAspGInLeuMeThyCySer	560
Db	1627	CTCGAATAAGATTAAGAACTCATGASAGAGAGCATTTGGACCAAAATTAAGATGTGTC	1686
Qy	561	MeThyGylLeuCYsLeuYsVaLYsAsnLLeaPLeuYsPheYsLLeIeVaLThRaLa	580
Db	1687	ATGTATGGCATTCGCAAGGTAAAGAAATTAAGACTTAAATTCATAATCATCTGACACGA	1746
Qy	581	ThYrLyAsPLeuProHsLaIvaLYaGInGluThThPheYsATgVaLLeuLLeYsGluGlu	600
Db	1747	TACAGAGATCTTCCATGAGCTGTCAGAGACATTTAAACGGTGTGATCAAGAAAGAG	1806
Qy	601	GluThYsAsPSeRLeIeVaLpHeThYsAnSerVaLPheMeGInaYgLeuYsThRaSn	620
Db	1807	GAGATGAGATTCAATTATAGATTTTATATACCTGCTTCATGACGAGAACTGAAGAAAT	1866
Qy	621	LLeuGInLYaLaSeThRaYgProProThLeuSerProIleProHsLLeProaY	640
Db	1867	ATTTTCAGATTAAGCTTCCACAGCGCCCTCCACTGTGTACCAAAATCCTCAATCTCTCCA	1926
Qy	641	SePProTYsLPhePProSeSerProLeuATgLIeProGlyGInaLLeYrLIeSer	660
Qy	1927	AGCCCTTAACAATTTCCATAGTTCACCTTACGGATTCCTGGAGGAAACATCTATATTTCA	1986
Qy	661	ProLeuYsSerProTYsLIeSeGluGlyLeuProThProThYsMeThPro	680
Db	1987	CCCTGGAAGGTCCATTAATAATTTTCGAAGGCTGSCACACCAACMAAATGATCTCA	2046
Qy	681	ArgSerThRGIleLeuVaSerLIeGlyLeuSerPheGlyThThSerGluYsPheGInLYs	700
Db	2047	AGATCAAGATCTTATGATCAATGTCATGATTCCTGGACTCTGAGAAATTCAGAA	2106
Qy	701	LLeaSGInMeVaLYsAsnSerAsPaYgVaLYaLYaYzArgSerLaLaGluGlySerAa	720
Db	2107	ATTAATATAGATGGTATGTAACAGGACCGGTGCTCAAAAGAAAGCTCGAGAGAACAC	2166
Qy	721	ProProLYsPProLeuYsLYsLeuArgPheAspLIeGluGlySerAspGluLaAspGly	740
Db	2167	CCCTCTAAACCATGAAAAAATCTCGCTTGATTAAGGAAGTCAAGTGAAGCAAGTGA	2226
Qy	741	SeRlySHsLeuProGlyLLeuSerLYsPheGInLYsLeuLaLaGluMeThRserThR	760
Db	2227	AGTAAACATCTCCAGAGAGAGTCCAAATTTTCACAGAAATCTGCAGAAATGACTTACT	2286
Qy	761	ArgThRaYgMeGInLYsGInLYsMeTaYsAsPSeMeThPThSerAaLYsGluGlu	780

QY 1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg 20
DB 112 ATGTCAGACACTGTTGAAGAAGTATGATGTTTCTACCTTCAGCAAAATGGAAGG 171
QY 21 ThrCysGluLeuLeuIleTyrLeuPheGlnProSerSerLysSerThrGluLeuAsnSer 40
DB 172 ACATGTGAACCTTATATTTGACACACCCAGGTCGATTCATCTACGAAATTAATCT 231
QY 41 AlaLeuValLeuLysValSerThrPheLeuLeuAlaLysGluValLeuGln 60
DB 232 GCATTGGGCTAAAGATTCTGGATCCATTTTATAGCTGAAGGAGATATACAA 291
QY 61 MetGluAspLeuValIleSerPheGlnLeuMetLeuLysValLeuAspThrPheIle 80
DB 292 ATGGAGATGATCGTGGATTCATTCTAGTTAATGCTATGCTCTTACATATTAT 351
QY 81 LysLeuSerProPheMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
DB 352 AAACCTCACCTCCATGCTGCTCAAGAACCATATAAAACAGCTGTATACCCATATAT 411
QY 101 GlysSerProArgThrProArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
DB 412 GGTTCACCTCGAACCACCCAGCCAGGTCAAGACAGAGCTGACGATACCAAAACACTA 471
QY 121 GluAsnAspThrArgIleIleGluValLeuLysGluLysGluLysAsnIleAspGlu 140
DB 472 GAAATATGATACAGAAATTTATGAAAGTCTCTGTATAGACATGAAATGTATATGATAG 531
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr 160
DB 532 GTGAAAAATGTTTATTTCAAAAAATTTTATACCTTTATGAATCTCTGAGCTGTATACA 591
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
DB 592 TCTAATGACATTCAGAGGTTGAAAAATCTTTCAACGATACGAAACAAATTTATCTTAAA 651
QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
DB 652 AATTAAGATCTAGATGCAAGATATTTTGGATCATGTATAACTCTGACGCTGATTCCT 711
QY 201 IleAspSerPheGluThrArgIleArgThrProArgLysSerAsnLeuAspGluValAsn 220
DB 712 ATAGCACTTTTGAAACACAGAGACACACGAAATTAACCTTCTGATCAAGAGTGAT 771
QY 221 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMet 240
DB 772 GTAATTCCTCCACACTCCAGTTAGAGCTGTTATGAACCTATCCACAAATTTAATGATG 831
QY 241 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnGly 260
DB 832 ATTTTAAATTCAGCAAGTATCAACTTCGAAATCTGATTCCTATTTTAAACAATGCTC 891
QY 261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 892 ACAGTGATCCAAAGAAAGATATACGAAAGATGAAAGATGAAAGATATACATCTTTAAA 951
QY 281 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
DB 952 GAGAAATTTGCTAAAGCTGTGGAGACAGCTTCTGTCCAAATTTGATACACAGCATACAA 1011
QY 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArg 320
DB 1012 CTTGAGAGTTCCTGTATACGAGATGAGATCCATGCTTAAATCATAGAGAGAGACGA 1071
QY 321 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
DB 1072 TTATTCATTTCAAAATTTTACCAAACTTTCGATGATGCAAACTTTTTCATATGCTTATATG 1131
QY 341 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
DB 1132 GCGTCGCGCTTTGAGGTTGTAATGCGCACATATACAGAAAGTACATCTCAGATCTGTAT 1191
QY 361 SerGlyThrAspLeuSerPheProThrIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
DB 1192 TCTGAGACAGATTTGCTTTCCATGATGATTCGATGATGGCTTAAATTTAAACCTTTAT 1251
QY 381 PheTyrLysValIleGluSerPheIleLysAlaGluGluLysLeuThrArgGluMetIle 400
DB 1252 TTTTCAAAAGTATGCAAACTTTTATCAAAAGCAGAAAGCAACTTGACAAAGAAATGATA 1311
QY 401 LysHisLeuGluArgCysGluLysArgIleMetGluSerLeuAlaThrPheLeuAspSer 420
DB 1312 AACCATTTGAAACATGTGAAATCATGAAATCATGAAATCCTTCTGATGCTCAGATTTCA 1371
QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGluProThrAspHisLeuGlu 440
DB 1372 CCTTATTTGATCTTATTAACATCAAAAGCCAGAGAGACCAACCTGATCACTCTGAA 1431
QY 441 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 460
DB 1432 TCTGCTTGTCTCTTAAATCTTCTCCAGAAATATACACTGACACAGATATGATCTT 1491
QY 461 SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn 480
DB 1492 TCTCCTGTAAAGTCTCCAAAGAAAAAGGTTCACTACGCTGAATTTCTACTGCAAT 1551
QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
DB 1552 GCAGAGACCAAGACACTCAGCTTCCAGACCCAGAAAGCATTTGAATCTACTCTCTT 1611
QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGlu 520
DB 1612 TCACGTGTTTAAAAAAAGTATGCGGTAGCGTATCGCGCTTAAATVACATCTTGATA 1671
QY 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrThrLeuPheGlnHisThr 540
DB 1672 CGGCTTCTGTGAGCACCCAGAAATTAGAACATATCACTGAGACCTTGTCCAGACACC 1731
QY 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetCysSer 560
DB 1732 CTCAGAAATGAGTATGACATCATGAGACAGCATTTGGACCAATTTATGATGTTTCC 1791
QY 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValAlaThrAla 580
DB 1792 ATGTATGGATATGCAAAAGTGAAGATATAGACCTTAATTCABAAATCATGTGAACACA 1851
QY 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGlu 600
DB 1852 TACAGGATCTTCTCATGCTGCTTCCAGAGACATTCAAACGCTTTTGATCAAGAGAGG 1911
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
DB 1912 GAGTATGATTTATATATATATATCTATTACTGGATTCATGACGAGACAGAAACAAAT 1971
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
DB 1972 ATTTTCAGTATGCTTCCACAGGCCCTTACCTGTACCAAAATCTCCATCTCTGCA 2031
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
DB 2032 AGCCCTTAAGTTTCCAGATTCACCTTACGATCTCTGGAGGAAACATCATATTTCA 2091
QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
DB 2092 CCCCAGAGATCATATTAATTAATTCAGAGGCTTCCCAACACCAACAAATATGATCCA 2151
QY 681 ArgSerArgIleLeuValSerIleGlyLysSerPheGlyThrSerGluLysPheGlnLys 700
DB 2152 AGATCAAGAAATCTAGATATCAATTTGATGATATTCGGGACCTTGTGAGAGTTCCAGAA 2211
QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGluSerAsn 720
DB 2212 ATTAATCAATATGATGAACAGACAGCCGTGCTCAAAAAAATGCTGAGAGAGCAAC 2271
QY 721 ProProLysProLeuLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly 740

QY	1	MeSerArgLeuLeuLysLysTrpAspValLeuPheAlaLeuPheSerLysLeuGluArg	20
Db	160	ATGCAAGACTGTTGGAAGAAGTATGATGTATTTGTTGGACCTTCAGCAAAATTGGAAAG	219
QY	21	ThrGsgLLeuLeuLeuLysTrpGlnProSerSerLysIleSerThrGluIleAsnSer	40
Db	220	ACATGTAACTTATATATTTTGGACACACACCACAGTGTGATTTCTACTGAAATTAATCT	279
QY	41	AlaLeuValLeuLysValSerTrpLleThrPheLeuLeuAlaLysGluValLeuGln	60
Db	280	GCATTTGGCTAAAGAGTTTCTTGATGATCATTTTATTAAGTAAAGGGAAGTATTCAA	339
QY	61	MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTrpPheIle	80
Db	340	ATGCAAGATGATCGTGGAATTCATTTCACTTAAAGTCATGTCTCTTCACTATTTATTT	399
QY	81	LysLeuSerProProMetLeuLeuLysGluProTrpLysThrAlaValIleProIleAsn	100
Db	400	AAACTCTACCTCCCAAGTGGTCTCAAGAACCATATAAACAGCTGTTATATCCATTAT	459
QY	101	GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGluLeu	120
Db	460	GGTTACCTCGCAACACCCAGCGAGGTGCAAGACAGAGTGCAGGATGCAAAACACTA	519
QY	121	GluAsnAspThrArgLleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu	140
Db	520	GAAATATGATACAAATAATTTGAAGTCTCTGTAAAGAACAAATAATGATATGATG	579
QY	141	ValLysAsnValLysPheLysAsnPheIleProPheMetAsnSerLeuGluLysValThr	160
Db	580	GTGAAATAATGTTATTTTCAAAATTTTATATCTTTATGAAATTCCTTGACCTGTAA	639
QY	161	SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTrpGluGluLleTrpLeuLys	180
Db	640	TCTATATGACCTCCAGAGGTTGAAAAATCTTCTAAACGATACGAAGAATTTATCTTAA	699
QY	181	AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer	200
Db	700	ATAAAGATGTACGATGCAAGATTTATTTTGGATCAAGATAAACCTTCAGACTGATCT	759
QY	201	IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluLysValAsn	220
Db	760	ATAGACATGTTTGAACACAGAGAACACACGAAAAAGTACCTTGATGAAAGGTGAT	819
QY	221	ValIleProProHisIleThrProValArgThrValMetAsnThrIleGlnIleuMetMet	240
Db	820	GTAATTTCTCCACACACCTCCAGTATGAGACGTTATGACACATATCCAACAATTAATGAT	879
QY	241	IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuLleSerTrpPheAsnAsnGys	260
Db	880	ATTTTAAATTCAGCAAGTACCAACCTTCAGAAATCTGTATTTCCATATTTTAAACAACGC	939
QY	261	ThrValAsnProLysGluSerIleLeuLysArgValLysAspLleGlyTrpLlePheLys	280
Db	940	ACAGAGTAATCCAAAGAAAGATATCTGAAAGAGCTGAAGATATAGGATATCATTTTAAA	999
QY	281	GluLysPheAlaLysAlaValaGlyGlnGlyCysValGluLleLysSerGlnArgTrpLys	300
Db	1000	GAGAAATTTGCTAAAGCTGTGGGACAGGGTGTGTGCAATTTGCATCACAGCATACAA	1059
QY	301	LeuGlyValArgLeuTrpTrpArgValMetGluSerMetLeuLysSerGluLysGluArg	320
Db	1060	CTTGAGCTTCCGCTGTATATACCGAGTATGGAATCCATCTCTTAAATCAAGAAAGAACGA	1119
QY	321	LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnLlePheHisMetSerLeuLeu	340
Db	1120	TATATCATTAATAATTTTATGCAAACTTCTGATATACAAACTTTTTCATATATGCTTTATG	1179
QY	341	AlaCysAlaLeuGluValaValMetAlaThrLysSerArgSerThrSerGlnAsnLeuAsp	360
Db	1180	GGCTGGCTCTTGAGAGTTGTATATGGCCACATATAGCAGAGTACATCTCAGATCTTGAT	1239

Qy	361	SerGlyThrAspLeuSerPheProTPIleLeuAsnValLeuAsnLeuLysAlaPheAsp	380
Db	1240	TCTGGACAGATGGTGTCTTCCATCGGATTCGAAAGTCCTTAATTTAAAGCCCTTGAT	1299
Qy	381	PheTyrLysValIleGluSerPheIleLysAlaGluLysValLeuThrArgIleuMetIle	400
Db	1300	TTTACAAAGGATCGAAAGTTTATCCAAAGCAGAAAGGCACTTACACAGAAATGATA	1359
Qy	401	LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer	420
Db	1360	AAACGTTTAGAAGCATGTGAACATCGATCATGGATCCCTTGATGGGTCCAGATATCA	1419
Qy	421	ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu	440
Db	1420	CCCTTATTTGATCTTATTTAAACATCAAGACCGAAGGAGCAACAATCATCCCTTGAA	1479
Qy	441	SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAspMetTyrLeu	460
Db	1480	TCTGGTTCCTCTTAATCTTCTCTCCAAATATACACTGCAGCATATGTATCTT	1539
Qy	461	SerProValArgSerProLysLysGlySerThrThrArgValAsnSerThrAlaAsn	480
Db	1540	TCTCTGTGAAGTCGCCAAGAAAGAAAGGTTCAACTACGGGTGTAATCTACTGCAAT	1599
Qy	481	AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu	500
Db	1600	GGAGAGACACAAAGCAACCTCGCCCTTCCACACCGAAGCAATGAAATCTACCTCTT	1659
Qy	501	SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu	520
Db	1660	TCACTGTTTATAAAAAGTTATCGCTTACCTTATCTCGGCTAAATACACTTTGTGA	1719
Qy	521	ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr	540
Db	1720	CGCCTTCTGTGAGACACCAGAAATTGAACATATCATCTGAGACCTTTTCCAGACACC	1779
Qy	541	LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer	560
Db	1780	CTGCAGAAATGAATAGCACTCATGAGACAGAGCAATTTGGACCAAAATTTGATGTGTTC	1839
Qy	561	MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleLeuAlaThrAla	580
Db	1840	ATGTATGGCAATTCGAAAGTAAAGTAAAGATTTACCTTTAAATTCAAATTCATGTACAGCA	1899
Qy	581	TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuLeuLysGluGln	600
Db	1900	TACAAAGATCTTCCATCATGCTTCCAGAGACATTCAAAGCTGTTTGAATCAAAAGAAAGG	1959
Qy	601	GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn	620
Db	1960	GAGTATGATTTATATATAGTATTCATATCAATCCGCTCTTCATGCAGAGACTGAAMAACAT	2019
Qy	621	IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg	640
Db	2020	ATTTCGATTAAGTCTTCACAGGCCCTTACCTTGACCAATATCTCATCTCTGCA	2079
Qy	641	SerProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSer	660
Db	2080	AGCCCTTAACAATTTCTAGTTCACCCCTTACGGATCTCGAAGGAACATCTATATTCCA	2139
Qy	661	ProLeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrPro	680
Db	2140	CCCTTCAAAAGATCCATATAAATTTCAAGAGGCTCGCCAACACCAACMAAAAGACTCCA	2199
Qy	681	ArgSerArgIleLeuValSerIleLysIleSerPheGlyThrSerGlyLysPheGlnLys	700
Db	2200	AGATCAAGATCTTATGTATCAATTTGTCAATCATTCGGACTTCTGAGAACTTCCAGAAA	2259
Qy	701	IleAsnGluMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysAsn	720
Db	2260	ATTAATCAATGTATGTACACGCAACGCTGTGCTCAAAAGAAAGTGTGTGAAGGAACAAAC	2319
Qy	721	ProProLysProLeuLysLysLeuArgPheAspIleGluLysSerAspGluAlaAspGly	740

```

|||||
Db 2320 CCTCTTAACCACTGAAAAAAGCTTTGATGATGTAAGATCATGATGAAAGCAAGATGCA 2379
Oy 741 SerIysHISLeuProGlyGluSerIysPheGlnGlnIysLeuAlaGluMetThrSerThr 760
Db 2380 AGTAAACATCTCCCGAGGAGATCCAAATTCAGCAAGAAACGCGAAGAAATGACTTACT 2439
Oy 761 ArgThrArgMetGlnIysGlnIysMetAsnAspSerMetAspThrSerAsnIysGluGlu 780
Db 2440 CGAACACGCAATGCAAAAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATG 2499,
Oy 781 Lys 781
Db 2500 AAA 2502

RESULT 14
AAV58443
ID AAV58443 standard; DNA: 3323 BP.
X 1
X 2 AAV58443:
X 3
X 4
X 5
X 6 02-DEC-1998 (first entry)
X 7
X 8 Modified retinoblastoma tumour suppressor gene.
X 9
X 10 Modified retinoblastoma tumour suppressor: R2SP protein; cancer therapy.
X 11
X 12 cellular proliferation inhibitor; ss.
X 13
X 14 Homo sapiens.
X 15
X 16
X 17 Key Location/Qualifiers
X 18 CDS 7..2562
X 19 FT /*tag= a
X 20
X 21
X 22
X 23
X 24
X 25
X 26
X 27
X 28
X 29
X 30
X 31
X 32
X 33
X 34
X 35
X 36
X 37
X 38
X 39
X 40
X 41
X 42
X 43
X 44
X 45
X 46
X 47
X 48
X 49
X 50
X 51
X 52
X 53
X 54
X 55
X 56
X 57
X 58
X 59
X 60
X 61
X 62
X 63
X 64
X 65
X 66
X 67
X 68
X 69
X 70
X 71
X 72
X 73
X 74
X 75
X 76
X 77
X 78
X 79
X 80
X 81
X 82
X 83
X 84
X 85
X 86
X 87
X 88
X 89
X 90
X 91
X 92
X 93
X 94
X 95
X 96
X 97
X 98
X 99
X 100
X 101
X 102
X 103
X 104
X 105
X 106
X 107
X 108
X 109
X 110
X 111
X 112
X 113
X 114
X 115
X 116
X 117
X 118
X 119
X 120
X 121
X 122
X 123
X 124
X 125
X 126
X 127
X 128
X 129
X 130
X 131
X 132
X 133
X 134
X 135
X 136
X 137
X 138
X 139
X 140
X 141
X 142
X 143
X 144
X 145
X 146
X 147
X 148
X 149
X 150
X 151
X 152
X 153
X 154
X 155
X 156
X 157
X 158
X 159
X 160
X 161
X 162
X 163
X 164
X 165
X 166
X 167
X 168
X 169
X 170
X 171
X 172
X 173
X 174
X 175
X 176
X 177
X 178
X 179
X 180
X 181
X 182
X 183
X 184
X 185
X 186
X 187
X 188
X 189
X 190
X 191
X 192
X 193
X 194
X 195
X 196
X 197
X 198
X 199
X 200
X 201
X 202
X 203
X 204
X 205
X 206
X 207
X 208
X 209
X 210
X 211
X 212
X 213
X 214
X 215
X 216
X 217
X 218
X 219
X 220
X 221
X 222
X 223
X 224
X 225
X 226
X 227
X 228
X 229
X 230
X 231
X 232
X 233
X 234
X 235
X 236
X 237
X 238
X 239
X 240
X 241
X 242
X 243
X 244
X 245
X 246
X 247
X 248
X 249
X 250
X 251
X 252
X 253
X 254
X 255
X 256
X 257
X 258
X 259
X 260
X 261
X 262
X 263
X 264
X 265
X 266
X 267
X 268
X 269
X 270
X 271
X 272
X 273
X 274
X 275
X 276
X 277
X 278
X 279
X 280
X 281
X 282
X 283
X 284
X 285
X 286
X 287
X 288
X 289
X 290
X 291
X 292
X 293
X 294
X 295
X 296
X 297
X 298
X 299
X 300
X 301
X 302
X 303
X 304
X 305
X 306
X 307
X 308
X 309
X 310
X 311
X 312
X 313
X 314
X 315
X 316
X 317
X 318
X 319
X 320
X 321
X 322
X 323
X 324
X 325
X 326
X 327
X 328
X 329
X 330
X 331
X 332
X 333
X 334
X 335
X 336
X 337
X 338
X 339
X 340
X 341
X 342
X 343
X 344
X 345
X 346
X 347
X 348
X 349
X 350
X 351
X 352
X 353
X 354
X 355
X 356
X 357
X 358
X 359
X 360
X 361
X 362
X 363
X 364
X 365
X 366
X 367
X 368
X 369
X 370
X 371
X 372
X 373
X 374
X 375
X 376
X 377
X 378
X 379
X 380
X 381
X 382
X 383
X 384
X 385
X 386
X 387
X 388
X 389
X 390
X 391
X 392
X 393
X 394
X 395
X 396
X 397
X 398
X 399
X 400
X 401
X 402
X 403
X 404
X 405
X 406
X 407
X 408
X 409
X 410
X 411
X 412
X 413
X 414
X 415
X 416
X 417
X 418
X 419
X 420
X 421
X 422
X 423
X 424
X 425
X 426
X 427
X 428
X 429
X 430
X 431
X 432
X 433
X 434
X 435
X 436
X 437
X 438
X 439
X 440
X 441
X 442
X 443
X 444
X 445
X 446
X 447
X 448
X 449
X 450
X 451
X 452
X 453
X 454
X 455
X 456
X 457
X 458
X 459
X 460
X 461
X 462
X 463
X 464
X 465
X 466
X 467
X 468
X 469
X 470
X 471
X 472
X 473
X 474
X 475
X 476
X 477
X 478
X 479
X 480
X 481
X 482
X 483
X 484
X 485
X 486
X 487
X 488
X 489
X 490
X 491
X 492
X 493
X 494
X 495
X 496
X 497
X 498
X 499
X 500
X 501
X 502
X 503
X 504
X 505
X 506
X 507
X 508
X 509
X 510
X 511
X 512
X 513
X 514
X 515
X 516
X 517
X 518
X 519
X 520
X 521
X 522
X 523
X 524
X 525
X 526
X 527
X 528
X 529
X 530
X 531
X 532
X 533
X 534
X 535
X 536
X 537
X 538
X 539
X 540
X 541
X 542
X 543
X 544
X 545
X 546
X 547
X 548
X 549
X 550
X 551
X 552
X 553
X 554
X 555
X 556
X 557
X 558
X 559
X 560
X 561
X 562
X 563
X 564
X 565
X 566
X 567
X 568
X 569
X 570
X 571
X 572
X 573
X 574
X 575
X 576
X 577
X 578
X 579
X 580
X 581
X 582
X 583
X 584
X 585
X 586
X 587
X 588
X 589
X 590
X 591
X 592
X 593
X 594
X 595
X 596
X 597
X 598
X 599
X 600
X 601
X 602
X 603
X 604
X 605
X 606
X 607
X 608
X 609
X 610
X 611
X 612
X 613
X 614
X 615
X 616
X 617
X 618
X 619
X 620
X 621
X 622
X 623
X 624
X 625
X 626
X 627
X 628
X 629
X 630
X 631
X 632
X 633
X 634
X 635
X 636
X 637
X 638
X 639
X 640
X 641
X 642
X 643
X 644
X 645
X 646
X 647
X 648
X 649
X 650
X 651
X 652
X 653
X 654
X 655
X 656
X 657
X 658
X 659
X 660
X 661
X 662
X 663
X 664
X 665
X 666
X 667
X 668
X 669
X 670
X 671
X 672
X 673
X 674
X 675
X 676
X 677
X 678
X 679
X 680
X 681
X 682
X 683
X 684
X 685
X 686
X 687
X 688
X 689
X 690
X 691
X 692
X 693
X 694
X 695
X 696
X 697
X 698
X 699
X 700
X 701
X 702
X 703
X 704
X 705
X 706
X 707
X 708
X 709
X 710
X 711
X 712
X 713
X 714
X 715
X 716
X 717
X 718
X 719
X 720
X 721
X 722
X 723
X 724
X 725
X 726
X 727
X 728
X 729
X 730
X 731
X 732
X 733
X 734
X 735
X 736
X 737
X 738
X 739
X 740
X 741
X 742
X 743
X 744
X 745
X 746
X 747
X 748
X 749
X 750
X 751
X 752
X 753
X 754
X 755
X 756
X 757
X 758
X 759
X 760
X 761
X 762
X 763
X 764
X 765
X 766
X 767
X 768
X 769
X 770
X 771
X 772
X 773
X 774
X 775
X 776
X 777
X 778
X 779
X 780
X 781
X 782
X 783
X 784
X 785
X 786
X 787
X 788
X 789
X 790
X 791
X 792
X 793
X 794
X 795
X 796
X 797
X 798
X 799
X 800
X 801
X 802
X 803
X 804
X 805
X 806
X 807
X 808
X 809
X 810
X 811
X 812
X 813
X 814
X 815
X 816
X 817
X 818
X 819
X 820
X 821
X 822
X 823
X 824
X 825
X 826
X 827
X 828
X 829
X 830
X 831
X 832
X 833
X 834
X 835
X 836
X 837
X 838
X 839
X 840
X 841
X 842
X 843
X 844
X 845
X 846
X 847
X 848
X 849
X 850
X 851
X 852
X 853
X 854
X 855
X 856
X 857
X 858
X 859
X 860
X 861
X 862
X 863
X 864
X 865
X 866
X 867
X 868
X 869
X 870
X 871
X 872
X 873
X 874
X 875
X 876
X 877
X 878
X 879
X 880
X 881
X 882
X 883
X 884
X 885
X 886
X 887
X 888
X 889
X 890
X 891
X 892
X 893
X 894
X 895
X 896
X 897
X 898
X 899
X 900
X 901
X 902
X 903
X 904
X 905
X 906
X 907
X 908
X 909
X 910
X 911
X 912
X 913
X 914
X 915
X 916
X 917
X 918
X 919
X 920
X 921
X 922
X 923
X 924
X 925
X 926
X 927
X 928
X 929
X 930
X 931
X 932
X 933
X 934
X 935
X 936
X 937
X 938
X 939
X 940
X 941
X 942
X 943
X 944
X 945
X 946
X 947
X 948
X 949
X 950
X 951
X 952
X 953
X 954
X 955
X 956
X 957
X 958
X 959
X 960
X 961
X 962
X 963
X 964
X 965
X 966
X 967
X 968
X 969
X 970
X 971
X 972
X 973
X 974
X 975
X 976
X 977
X 978
X 979
X 980
X 981
X 982
X 983
X 984
X 985
X 986
X 987
X 988
X 989
X 990
X 991
X 992
X 993
X 994
X 995
X 996
X 997
X 998
X 999
X 1000
X 1001
X 1002
X 1003
X 1004
X 1005
X 1006
X 1007
X 1008
X 1009
X 1010
X 1011
X 1012
X 1013
X 1014
X 1015
X 1016
X 1017
X 1018
X 1019
X 1020
X 1021
X 1022
X 1023
X 1024
X 1025
X 1026
X 1027
X 1028
X 1029
X 1030
X 1031
X 1032
X 1033
X 1034
X 1035
X 1036
X 1037
X 1038
X 1039
X 1040
X 1041
X 1042
X 1043
X 1044
X 1045
X 1046
X 1047
X 1048
X 1049
X 1050
X 1051
X 1052
X 1053
X 1054
X 1055
X 1056
X 1057
X 1058
X 1059
X 1060
X 1061
X 1062
X 1063
X 1064
X 1065
X 1066
X 1067
X 1068
X 1069
X 1070
X 1071
X 1072
X 1073
X 1074
X 1075
X 1076
X 1077
X 1078
X 1079
X 1080
X 1081
X 1082
X 1083
X 1084
X 1085
X 1086
X 1087
X 1088
X 1089
X 1090
X 1091
X 1092
X 1093
X 1094
X 1095
X 1096
X 1097
X 1098
X 1099
X 1100
X 1101
X 1102
X 1103
X 1104
X 1105
X 1106
X 1107
X 1108
X 1109
X 1110
X 1111
X 1112
X 1113
X 1114
X 1115
X 1116
X 1117
X 1118
X 1119
X 1120
X 1121
X 1122
X 1123
X 1124
X 1125
X 1126
X 1127
X 1128
X 1129
X 1130
X 1131
X 1132
X 1133
X 1134
X 1135
X 1136
X 1137
X 1138
X 1139
X 1140
X 1141
X 1142
X 1143
X 1144
X 1145
X 1146
X 1147
X 1148
X 1149
X 1150
X 1151
X 1152
X 1153
X 1154
X 1155
X 1156
X 1157
X 1158
X 1159
X 1160
X 1161
X 1162
X 1163
X 1164
X 1165
X 1166
X 1167
X 1168
X 1169
X 1170
X 1171
X 1172
X 1173
X 1174
X 1175
X 1176
X 1177
X 1178
X 1179
X 1180
X 1181
X 1182
X 1183
X 1184
X 1185
X 1186
X 1187
X 1188
X 1189
X 1190
X 1191
X 1192
X 1193
X 1194
X 1195
X 1196
X 1197
X 1198
X 1199
X 1200
X 1201
X 1202
X 1203
X 1204
X 1205
X 1206
X 1207
X 1208
X 1209
X 1210
X 1211
X 1212
X 1213
X 1214
X 1215
X 1216
X 1217
X 1218
X 1219
X 1220
X 1221
X 1222
X 1223
X 1224
X 1225
X 1226
X 1227
X 1228
X 1229
X 1230
X 1231
X 1232
X 1233
X 1234
X 1235
X 1236
X 1237
X 1238
X 1239
X 1240
X 1241
X 1242
X 1243
X 1244
X 1245
X 1246
X 1247
X 1248
X 1249
X 1250
X 1251
X 1252
X 1253
X 1254
X 1255
X 1256
X 1257
X 1258
X 1259
X 1260
X 1261
X 1262
X 1263
X 1264
X 1265
X 1266
X 1267
X 1268
X 1269
X 1270
X 1271
X 1272
X 1273
X 1274
X 1275
X 1276
X 1277
X 1278
X 1279
X 1280
X 1281
X 1282
X 1283
X 1284
X 1285
X 1286
X 1287
X 1288
X 1289
X 1290
X 1291
X 1292
X 1293
X 1294
X 1295
X 1296
X 1297
X 1298
X 1299
X 1300
X 1301
X 1302
X 1303
X 1304
X 1305
X 1306
X 1307
X 1308
X 1309
X 1310
X 1311
X 1312
X 1313
X 1314
X 1315
X 1316
X 1317
X 1318
X 1319
X 1320
X 1321
X 1322
X 1323
X 1324
X 1325
X 1326
X 1327
X 1328
X 1329
X 1330
X 1331
X 1332
X 1333
X 1334
X 1335
X 1336
X 1337
X 1338
X 1339
X 1340
X 1341
X 1342
X 1343
X 1344
X 1345
X 1346
X 1347
X 1348
X 1349
X 1350
X 1351
X 1352
X 1353
X 1354
X 1355
X 1356
X 1357
X 1358
X 1359
X 1360
X 1361
X 1362
X 1363
X 1364
X 1365
X 1366
X 1367
X 1368
X 1369
X 1370
X 1371
X 1372
X 1373
X 1374
X 1375
X 1376
X 1377
X 1378
X 1379
X 1380
X 1381
X 1382
X 1383
X 1384
X 1385
X 1386
X 1387
X 1388
X 1389
X 1390
X 1391
X 1392
X 1393
X 1394
X 1395
X 1396
X 1397
X 1398
X 1399
X 1400
X 1401
X 1402
X 1403
X 1404
X 1405
X 1406
X 1407
X 1408
X 1409
X 1410
X 1411
X 1412
X 1413
X 1414
X 1415
X 1416
X 1417
X 1418
X 1419
X 1420
X 1421
X 1422
X 1423
X 1424
X 1425
X 1426
X 1427
X 1428
X 1429
X 1430
X 1431
X 1432
X 1433
X 1434
X 1435
X 1436
X 1437
X 1438
X 1439
X 1440
X 1441
X 1442
X 1443
X 1444
X 1445
X 1446
X 1447
X 1448
X 1449
X 1450
X 1451
X 1452
X 1453
X 1454
X 1455
X 1456
X 1457
X 1458
X 1459
X 1460
X 1461
X 1462
X 1463
X 1464
X 1465
X 1466
X 1467
X 1468
X 1469
X 1470
X 1471
X 1472
X 1473
X 1474
X 1475
X 1476
X 1477
X 1478
X 1479
X 1480
X 1481
X 1482
X 1483
X 1484
X 1485
X 1486
X 1487
X 1488
X 1489
X 1490
X 1491
X 1492
X 1493
X 1494
X 1495
X 1496
X 1497
X 1498
X 1499
X 1500
X 1501
X 1502
X 1503
X 1504
X 1505
X 1506
X 1507
X 1508
X 1509
X 1510
X 1511
X 1512
X 1513
X 1514
X 1515
X 1516
X 1517
X 1518
X 1519
X 1520
X 1521
X 1522
X 1523
X 1524
X 1525
X 1526
X 1527
X 1528
X 1529
X 1530
X 1531
X 1532
X 1533
X 1534
X 1535
X 1536
X 1537
X 1538
X 1539
X 1540
X 1541
X 1542
X 1543
X 1544
X 1545
X 1546
X 1547
X 1548
X 1549
X 1550
X 1551
X 1552
X 1553
X 1554
X 1555
X 1556
X 1557
X 1558
X 1559
X 1560
X 1561
X 1562
X 1563
X 1564
X 1565
X 1566
X 1567
X 1568
X 1569
X 1570
X 1571
X 1572
X 1573
X 1574
X 1575
X 1576
X 1577
X 1578
X 1579
X 1580
X 1581
X 1582
X 1583
X 1584
X 1585
X 1586
X 1587
X 1588
X 1589
X 1590
X 1591
X 1592
X 1593
X 1594
X 1595
X 1596
X 1597
X 1598
X 1599
X 1600
X 1601
X 1602
X 1603
X 1604
X 1605
X 1606
X 1607
X 1608
X 1609
X 1610
X 1611
X 1612
X 1613
X 1614
X 1615
X 1616
X 1617
X 1618
X 1619
X 1620
X 1621
X 1622
X 1623
X 1624
X 1625
X 1626
X 1627
X 1628
X 1629
X 1630
X 1631
X 1632
X 1633
X 1634
X 1635
X 1636
X 1637
X 1638
X 1639
X 1640
X 1641
X 1642
X 1643
X 1644
X 1645
X 1646
X 1647
X 1648
X 1649
X 1650
X 1651
X 1652
X 1653
X 1654
X 1655
X 1656
X 1657
X 1658
X 1659
X 1660
X 1661
X 1662
X 1663
X 1664
X 1665
X 1666
X 1667
X 1668
X 1669
X 1670
X 1671
X 1672
X 1673
X 1674
X 1675
X 1676
X 1677
X 1678
X 1679
X 1680
X 1681
X 1682
X 1683
X 1684
X 1685
X 1686
X 1687
X 1688
X 1689
X 1690
X 1691
X 1692
X 1693
X 1694
X 1695
X 1696
X 1697
X 1698
X 1699
X 1700
X 1701
X 1702
X 1703
X 1704
X 1705
X 1706
X 1707
X 1708
X 1709
X 1710
X 1711
X 1712
X 1713
X 1714
X 1715
X 1716
X 1717
X 1718
X 1719
X 1720
X 1721
X 1722
X 1723
X 1724
X 1725
X 1726
X 1727
X 1728
X 1729
X 1730
X 1731
X 1732
X 1733
X 1734
X 1735
X 1736
X 1737
X 1738
X 1739
X 1740
X 1741
X 1742
X 1743
X 1744
X 1745
X 1746
X 1747
X 1748
X 1749
X 1750
X 1751
X 1752
X 1753
X 1754
X 1755
X 1756
X 1757
X 1758
X 1759
X 1760
X 1761
X 1762
X 1763
X 1764
X 1765
X 1766
X 1767
X 1768
X 1769
X 1770
X 1771
X 1772
X 1773
X 1774
X 1775
X 1776
X 1777
X 1778
X 1779
X 1780
X 1781
X 1782
X 1783
X 1784
X 1785
X 1786
X 1787
X 1788
X 1789
X 1790
X 1791
X 1792
X 1793
X 1794
X 1795
X 1796
X 1797
X 1798
X 1799
X 1800
X 1801
X 1802
X 1803
X 1804
X 1805
X 1806
X 1807
X 1808
X 1809
X 1810
X 1811
X 1812
X 1813
X 1814
X 1815
X 1816
X 1817
X 1818
X 1819
X 1820
X 1821
X 1822
X 1823
X 1824
X 1825
X 1826
X 1827
X 1828
X 1829
X 1830
X 1831
X 1832
X 1833
X 1834
X 1835
X 1836
X 1837
X 1838
X 1839
X 1840
X 1841
X 1842
X 1843
X 1844
X 1845
X 1846
X 1847
X 1848
X 1849
X 1850
X 1851
X 18
```

```

Qy 361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuValAlaPheAsp 380
    |||
Db 1297 TCGGAAACGAGTATTTCTTTCCCATGATTCGATGCTTAATTTAAAGCCCTTGAT 1356
Qy 381 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
    |||
Db 1357 TTTTAAAGATGATCGAAGATTTTATCAAGACAGAGACCTGACAAAGAAATATATA 1416
Qy 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer 420
    |||
Db 1417 AACCATTTGAGACGATGGAACATCGATCATGGAATCCCTTGACATGCGCTCGAGATTTCA 1476
Qy 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
    |||
Db 1477 CCTTTATTGATCTTATTAAACATCAAGACCGAAGACGAGACCAATGATCCTTGAA 1536
Qy 441 SerAlaCysPProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetCysLeu 460
    |||
Db 1537 TCTGCTTGCTGCTTAATCTCTCTCCAGAAATTAATCACTGACAGCATATGATCTTT 1596
Qy 461 SerProValArgSerProLysLysLysGlySerThrArgValAsnSerThrAlaAsn 480
    |||
Db 1597 TCTCTGTAAGATCTCCAAAGAAAAAGTTCAACTACCGCTGTAATTTCTACTGCAAT 1656
Qy 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
    |||
Db 1657 GCGAGACACACAGACACCTCAGCTTCCAGACCCAGAACCAATTAATCTACTCTCTT 1716
Qy 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu 520
    |||
Db 1717 TCACTGTTTTTAAAAAAAGTATCGGCTAGCCCTATCTCCGGCTAAATACACTTTGGAA 1776
Qy 521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr 540
    |||
Db 1777 CGCCTTCTGTCGACACCCAGAAATAGAACATATCATCTGAGCCCTTTCAGACACCC 1836
Qy 541 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
    |||
Db 1837 CTCGACAAATGATATGAACCTCATAGAGACAGCATTGGACCAATTTATGATGTCTCC 1896
Qy 561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValIleThrAla 580
    |||
Db 1897 ATGTATGCGCATATGCAAAAGTAAAGATATAGACCTTAATTAATCAATCTGTAAACGCA 1956
Qy 581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
    |||
Db 1957 TACAAAGATCTCTCATGCTGTCAGAGACATTCAAACGATGTTTGTATCAAGAAAGAG 2016
Qy 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
    |||
Db 2017 GAGTATGATCTTATATAGTATTTCTATAACTCGGTCTTCATGCAAGACTGAACCAAT 2076
Qy 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
    |||
Db 2077 ATTTCGACATATGCTTCACACAGGCCCTTACCTTGTCACCAATACCTCAATTCCTCGA 2136
Qy 641 SerProTyrLysPheProSerSerProLeuArgIleProGluGlyAsnIleTyrIleSer 660
    |||
Db 2137 AGCCCTTACAAAGTTCTAGTTACCCCTTAGGATTCCTGAGAGGACATCATATTTTCA 2196
Qy 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
    |||
Db 2197 CCCCTGAAGTCCATATTAATTTTCAGAAAGTCTGCAACACCAAAATATGATCTCA 2256
Qy 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
    |||
Db 2257 AGATTCAGAGATCTAGTATCAATATGGTGAATCATTTGGGGACCTTCGAGAACTCCAGAAA 2316
Qy 701 IleAsnGlnMetValCysAsnSerAspArgValIleLeuLysArgSerAlaGluGlySerAsn 720
    |||
Db 2317 ATAAATCAATGATGTATGTAAACAGGACGACGATGTGCTAAAAGAAAGTCTCAAGAGAAC 2376
Qy 721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGlnAlaAspGly 740

```

```

Db 2237 CCGCTTAACACGATGAAAAACACGCTTTGATATGAAAGATCGATGAAACGAGATGGA 2436
Qy 741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
    |||
Db 2437 AGTAAACATCTCCAGAGACTCCAAATTTCCAGCAAACTGCGAGAAATATGATCTTACT 2496
Qy 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
    |||
Db 2497 CGAACACGAAATCAAAACAGCAAAATGAAATGATGATGATGATCTCAAAACAGAAAG 2556
Qy 781 Lys 781
Db 2557 AAA 2559

RESULT 15
AAV58446 standard; DNA; 3323 BP.
ID AAV58446
AC AAV58446;
XX
XX 02-DEC-1998 (first entry)
XX
XX Modified retinoblastoma tumour suppressor gene.
DE Modified retinoblastoma tumour suppressor; RFP protein; cancer therapy;
KM Modified retinoblastoma tumour suppressor; RFP protein; cancer therapy;
KN cellular proliferation inhibitor; ss.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 7..2562
FT CDS /*tag= a
XX
XX MO9837091-A2.
XX
XX 27-AUG-1998.
XX
XX 19-FEB-1998; 98MO-US03041.
XX
XX 20-FEB-1997; 97US-0038118.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Benedict WF, Hu S, Xu H, Zhou Y;
XX
XX WPI: 1998-480788/41.
XX
XX P-PSDB; AAV69370.
XX
XX
XX Retinoblastoma suppressor protein with N-terminal modification -
XX Inhibiting cellular proliferation, particularly cancer
XX
XX Claim 22: Page 180-184; 249pp; English.
XX
XX This sequence encodes a modified retinoblastoma tumour suppressor
XX protein (RFP) of the invention. The proteins can be used for inhibiting
XX cellular proliferation, when coadministered with a p53 protein. The RFPs
XX can be used for treating diseases characterised by abnormal cellular
XX proliferation, particularly cancers. The RFPs have a broader spectrum of
XX activity than wild type RFPs.
XX
XX Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 0
XX Score: 4017.00
XX Length: 3323
XX Percent Similarity: 100.00%
XX Matches: 781
XX Best Local Similarity: 100.00%
XX Conservative: 0
XX Mismatches: 0
XX Query Match: 100.00%
XX Indels: 0
XX DB: 19
XX
XX US-09-026-459a-37 (1-781) x AAV58446 (1-3323)

```

Oy	1	MeSerAsgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuLjunc	20
Db	217	ATGTCAACAGCTTTGMAAGAGATGATGATTTCTTGACCTTCAGCAAAATTGMAAG	276
Oy	21	ThrCysGluLeuLeuLeuTyrLeuThrGlnProSerSerSerLysSerGlnLeuSer	40
Db	277	ACGTGTGAACCTTAATATTTTGACACACACCACAGCTTGATCTGCAAAATAATCT	336
Oy	41	AlaLeuValLeuLysValSerTrpLethrPheLeuAlaLysGluValLeuGln	60
Db	337	GCATTGTGCTCAAAAGTTCTTGACACACATTTTATAGCTTAAAGGAGACTTATCA	396
Oy	61	MetGluAspAspLeuValLieserPheGlnLeuMetLeuCysValLeuAspTyrPheLe	80
Db	397	ATGGAAAGATGATCTGTGATTTCAATTTCAGTTAAAGCATGTGTGCTGTGATTTTAT	456
Oy	81	LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValLeuProLeuSn	100
Db	457	AAACTCTCCACCTCCATGTTGCTCAAGAACCATTTAAACAGCTGTATTACCCATAT	516
Oy	101	GlySerProArgThrProAlaGArgGlyGlnAsnArgSerAlaArgLeuAlaLysGlnLeu	120
Db	517	GGTTCCACCTCGAACACCCAGGCGAGTCGAACAAGCATGCGACGATAGCAAAACACTA	576
Oy	121	GluAsnAspThrArgLilelleGluValLeuCysLysGluLysGluCysAsnLiespGlu	140
Db	577	GAAATGATACAGATATTATTGAAAGTTCTCTGTAAAGACATGATGTATATATAGTAG	636
Oy	141	ValLysAsnValTyrPheLysAsnPhelLeuProPheMetAsnSerLeuGlyLeuValThr	160
Db	637	GTCAAAAGATTTATTTCTCAAAATTTATACCTTTATGATTTCTGTGACTTGTAA	696
Oy	161	SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluLjuncLeuLys	180
Db	697	TCTAAAGGACTTCCAGAGGTGTGAAATCTTTTAAACATTCGAAAGAAATTTATCTTAA	756
Oy	181	AsnLysAspLeuAspAlaArgLeuPheLeuAspPheLysPheLysGlnThrAspSer	200
Db	757	ATTTAAAGATCTGATGACGAATTTATTTTGGATCTATGATTAACCTTCCAGACTATCT	816
Oy	201	LieserPheGluThrGlnArgThrProAlaGlySerAsnLeuAspGluGluValAsn	220
Db	817	ATGACAGTTTTGAAACACAGACACACACCAAAATAACCTTATGTAAGAGGTGAT	876
Oy	221	ValLeuProProLisThrProValArgThrValMetAsnThrLleGlnLeuMetLeu	240
Db	877	GTAATTCCCTCCACACACACAGTACGACTGTATTGAACAACATACCAACATTAATGAG	936
Oy	241	LleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuLieserTyrPheAsnAsnCys	260
Db	937	ATTTTAAATTTCGCAAGTATCAACTCTCAGAAATCTGATTTCTATTTTAAACAATGC	996
Oy	261	ThrValAsnProLysGluSerLleLeuLysArgValLysAspLleGlyTyrLlePheLys	280
Db	997	ACAGTAACTCCAAAGAAAGATGATCTGCAAAAGTGAAGGATATAGATATCATCTTTAA	1056
Oy	281	GluLysPheAlaLysAlaValAlaGlyGlnGlyCysValGluLleGlySerGlnArgTyrLys	300
Db	1057	GAGAAATTTGGCTPAAAGCTGTGGGACAGGGGTGTGTGCAAAATTTGGATACAGCATPACAA	1116
Oy	301	LeuGluValArgLeuTyrTyrArgValLleMetGluSerMetLeuLysSerGluGluGluArg	320
Db	1117	CTTGAGAGTTCCGCTTATTTACCGATPAAAGAAATCCATTCATTAAATCAGAAAGACAGA	1176
Oy	321	LeuSerLleGlnAsnPheSerLysLeuLeuAsnAspAsnLlePheLisMetSerLeuLeu	340
Db	1177	TTATCATTCACAAATTTTACGCAAACTTCGATGACCAACATTTTTCATATGCTTTATTC	1236
Oy	341	AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp	360
Db	1237	GCCTGGCGCTTGGAGGTGTATATGGCCACATATATACAGAAATATCATCTCGAATCTTGAT	1296

QY	361	SGCLYTHAASPLEUSERPHROTPDILELAAENVLLEAENLEUYSALAPHEAS	380
Db	1297	TCGGACAGATTTCTCTTCCATGGATTCTGATGCTTAATTTAAAGCCTTGAT	1356
QY	381	PhenyllysValIleGluSerPheIleYsAlaGluGlyAsnLeuThrArgIleUctIle	400
Db	1357	TTTTAACAAAGATGATGAAAGTTTTATCAAGACGAAGGCAACTTGCAAGAAAGATA	1416
QY	401	LYSHILEAGLILARYCSGLNHLSARGILEMETGLUSERLEUALATPLEUSERASPSER	420
Db	1417	AACATTATGACGATGGAACATCGAATCTGGAATCCCTGCATGGCTCTCATATCA	1476
QY	421	ProteinPhasPLEULEIYSGILSERLYSAPARAGGUGLYPROTHRAPHSILEUGIL	440
Db	1477	CGTTATTTGATGCTTATTAACAAATCAAGAGACCGAGAGAGCCAACTGATCACTTGAA	1536
QY	441	SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHISThrAlaIAsnMetYrLeu	460
Db	1537	TCGCTGTGCTCTTAATCTTCCTCCAGAAATACACACTGGACGAGTAATGATTCAT	1596
QY	461	SerProValArgSerProLYsLYSGILSerThrThrArgValAsnSerThrAlaAsn	480
Db	1597	TCCTCGTAAAGATCTCCAAAGAAAAAGGTCTACAGCGGTAAATCTACTGCAAT	1656
QY	481	ALAGLUTHGILALATHSERALAPHGLINTHGLINYSPROLYSSEPTHSERLEU	500
Db	1657	GCGAAGACACAAAGCACTCGCTTCCAAAGCCCAAGCACTTGAATCTACTCTCTT	1716
QY	501	SerLeuPheYrLYsLYsValYrArgLYsAlaYrLeuArgLYsAsnThrLeuCYSGIL	520
Db	1717	TCACGTGTTTTATAAAAAGTATATCGGCTACGCTACCTACCTCCGGCAAAATACACTTGTGAA	1776
QY	521	ArgLeuLeuSerGlnHISProGlnLeuGlnNHLSILEILETPRThrLeuPheGlnHISThr	540
Db	1777	CGCCTTCTGTGACACCCCGAATTTGAACATATCATCTGGACCCTTTCCAGCACACC	1836
QY	541	LeuGlnAsnGluThrYsGlnLeuMetArgASPARGHISLEAARGINILEMETMetCysSer	560
Db	1837	CTCGAGATGATGATGAACTCATAGAGACAGGCACTTGGACCAAAATTAAGATGTCTCC	1896
QY	561	MethylGLYLecLYsLYsValLYsAsnIAsnPLEULYSPhelYsILEILEVALThrAla	580
Db	1897	ATGATAGCCATATGCAAAAGTAAAGATATGACCTTAAATTCAAAAATCATTTGTAACAGCA	1956
QY	581	TYrLYsAspLeuProHISAlaValAlaGlnGluThrPheLYsArgValLEULEIYSGILGlu	600
Db	1957	TACAGAGATCTCCATCATGCTGCTTCAGAGACATCTCAAGCGTTGTGATCAAGAAAGAG	2016
QY	601	GluThrAspSerILEILEVALPheYrAsnSerValPheMetGlnArgLYsLYsThrAsn	620
Db	2017	GAGATGATCTTATTAAGTATCTTATTAACCTGGGCTTCTATGACAGACNCTAAACAAAT	2077
QY	621	ILEuGlnIlyrAlaSerThrArgProProThrLeuSerProIleProHISILEProArg	640
Db	2077	ATTTTGGAGATGCTTCCACACGAGCCGCCCTTACACCAATPACCCTCAATCTCTGCA	2136
QY	641	SerProYrLYsPheProSerSerProLeuArgILEProGILYsAsnILEYrILESer	660
Db	2137	AGCCCTTACAAAGTTCTCTAGTTCAACCTTACGAGATCTCGGAGGGAACATCTAATTTCA	2196
QY	661	ProLeuLYsSerProYrLYsILESerGluLYsLeuProThrProThrLYsMetThrPro	680
Db	2197	CCCTGAGAGGTCCATATAAAATTTCCAAAGGCTCCCAACACCAACAAATAATGACTCCA	2256
QY	681	ArgSerArgILEuValSerILEGILYsSerPheGILYrThrSerGILYsPheGILYs	700
Db	2257	AGATCAACAATCTAGTATCAATATGGGAATTCATTCGGCACTTCGAGAAAGTCCAGAAA	2316
QY	701	ILEAsnIlyMetValCysAsnSerAspArgValLEuLYsArgSerAlaGILYsSerAsn	720
Db	2317	ATAAATCAGATGATATGATACAGGACCGACTGCTCTAAAGAAAGTCTGAAGAGAACAAAC	2376
QY	721	ProProLYsProLeuLYsLYsLeuArgPheAspIILEGILYsSerAspGILuAlaAspGILY	740

Db 2377 |||||
CCTCCTAAACCACTGAAAACTACCTTGATATGTAAGCATCAGATCAAGCAGATGA 2436
QY 741 SerLysHisLeuProGlySerLysPheGlnLysLeuAlaGluMetThrSerThr 760
Db 2437 AGTAACATCTCCCGAGAGAGTCCAAATTTCACGAGAACTGGCAAAATGACTTCTACT 2496
QY 761 ArgThrArgMetGlnLysGlnLysMetAsnASPSetMetAspThrSerAsnLysGluGlu 780
Db 2497 CGAACACGAAATGCAAAAGCAAAATGAAATGATAGCATGATACCTCAACCAAGGAAAG 2556
QY 781 Lys 781
Db 2557 AAA 2559

Search completed: January 18, 2003, 08:41:34
Job time : 305.854 secs

